IN THE UNITED STATES DISTRICT COURT

FOR THE WESTERN DISTRICT OF MICHIGAN

SOUTHERN DIVISION

UNITED STATES OF AMERICA,

Plaintiff, No. 1:17cr130

vs.

DANIEL GISSANTANER,

Defendant.

Before:

THE HONORABLE JANET NEFF,
U.S. District Judge
Grand Rapids, Michigan
Monday, July 8, 2019
Daubert Hearing Proceedings

APPEARANCES:

MR. ANDREW BIRGE, U.S. ATTORNEY
By: MR. JUSTIN MATTHEW PRESANT
330 Ionia Avenue, NW
P.O. Box 208
Grand Rapids, MI 49501-0208
(616) 808-2184

On behalf of the Plaintiff;

FEDERAL PUBLIC DEFENDERS
By: MS. JOANNA KLOET
MR. PEDRO CELIS
MS. HELEN NIEUWENHUIS
50 Louis Street, Suite 300
Grand Rapids, MI 49503-2633
(616) 742-7420

On behalf of the Defendant.

Also Present: Jenny Norton and Emily Seale.

REPORTED BY: MR. PAUL G. BRANDELL, CSR-4552, RPR

07/08/2019

(Proceedings, 9:08 a.m.)

THE CLERK: The United States District Court for the Western District of Michigan, the Honorable Janet T. Neff, United States District Judge, presiding. Court is now in session. Please be seated.

THE COURT: Good morning, everybody. This is the date and time set for a continuation of a Daubert hearing which commenced about a year ago, and since then we have explored some of the very technical aspects of probabilistic genotyping, and today we are going to hear from two very imminent experts in that area. And just to have a little bit of a cautionary note to counsel, I have read, reread what I consider to be the most important material we gathered last year. And I have read pretty closely the two reports that were submitted by Dr. Coble and Dr. Krane, so I am hopeful that you will keep that in mind as you go through your questioning and presentation of evidence.

I see we have extensive evidence books here on the bench for me, which of course, I haven't had a chance to look at because they just came this morning, but please do focus your presentations on the issues that I asked the two experts to address in their reports, which they have.

It's my intention, after hearing everything today and then having an opportunity to review the exhibits which you

have provided, to have a written opinion for you soon.

Okay. With that, let's get started. I think we are going to start the testimony with Dr. Coble, correct, Mr. Presant?

MR. PRESANT: Whatever the Court pleases.

THE COURT: Yes, please.

I beg your pardon. I forgot to ask for appearances for the record. Counsel, would you please put your appearances on the record.

Thank you, Paul.

MR. PRESANT: Your Honor, Justin Presant for the United States. With me this morning is Jenny Norton from the U.S. Attorney office who will be assisting with exhibits.

MS. KLOET: Good morning, Your Honor. Joanna Kloet on behalf of Mr. Gissantaner, who is seated three individuals to my left, along with Pedro Celis and Helen Nieuwenhuis, along with Emily Seale.

MICHAEL DEWITT COBLE, GOVERNMENT

having been first duly sworn, testified as follows:

(Witness sworn, 9:12 a.m.)

THE CLERK: Please take a seat at the witness stand and state your name and spell your last name for the record.

THE WITNESS: My name is Michael Dewitt, D-e-w-i-t-t, Coble, C-o-b, as in boy, l-e.

THE COURT: Mr. Presant?

MR. PRESANT: Your Honor, is it the Court's intention for me to examine Mr. Coble first?

THE COURT: Yes. It is. I suppose I should have had a little additional explanation. This is a bit of an unusual circumstance for me. I haven't had the -- you know, had additional experts in a case like this in the past. I just think that because the evidence is being offered by the government it is for the government to defend it, so I would prefer that you go first on examining the witnesses. And unless there is a challenge to the expertise of the witnesses, I wouldn't spend a lot of time going through that.

I have Dr. Coble's curriculum vitae. I think I probably have Dr. Krane's from some time ago, but in any event, unless there is a challenge to the expertise of either of these men, which I can't imagine what it would be, don't spend a whole lot of time on qualifications. Okay?

MR. PRESANT: Very well, Your Honor. As the court knows, because of the bar on ex parte communications I have not talked to Dr. Coble about his report, so I don't have a lengthy examination prepared for him today. I have a few questions for him.

THE COURT: Did you take his deposition?

MR. PRESANT: I did not. No.

THE COURT: Did you take Dr. Krane's deposition?

MR. PRESANT: I did. Yes.

THE COURT: Okay. Okay. And Defense counsel did not depose Dr. Coble?

MR. PRESANT: That's correct.

THE COURT: Okay.

MR. PRESANT: Both parties noticed depositions of both experts, but after reviewing the reports there were some adjustments to the parties' view of the necessity of depositions.

THE COURT: Well, I will have some questions, and once you are done and once Ms. Kloet is done I will have some questions going forward.

MR. PRESANT: Thank you, Your Honor.

DIRECT EXAMINATION

BY MR. PRESANT:

Q Good morning, Dr. Coble.

A Good morning.

Q Dr. Coble, I am going to skip over your qualification entirely because the government has no challenges to those in accordance with the Court's instruction. So let's just go straight to your report. Do you have a copy of your report with you?

A Unfortunately I don't. I left it at the hotel in my luggage.

Q No problem at all.

MR. PRESANT: May I approach, Your Honor?

THE COURT: Yes.

THE WITNESS: Thank you.

MR. PRESANT: Your Honor, would it assist the Court if we brought up an electronic version of the report?

THE COURT: I don't need it but somebody else might. Maybe Dr. Coble would or maybe counsel for the Defense might, so that's fine.

MR. PRESANT: Let's bring up the report to have in case we need it.

BY MR. PRESANT:

Q So Dr. Coble, would you start just by describing what you did to prepare this report after the Court engaged you as an expert?

A So I was provided with the transcripts of both days. So I read through both of those transcripts, and in addition to that, all of the exhibits, both from the government and from the Defense, and so I read through all of those, also.

Q And what was your primary conclusion regarding the work done by the Michigan State Police in this case?

A I felt as I mention on -- let's see, on the No. 5, the application of STRmix in this case -- this is on the last page of my report. I did review the electropherograms that were provided of the evidence. I did look at the outputs from STRmix, and the report from the Michigan State Police, and of course, reviewing the testimony from Ms. Smith regarding this

report. And I feel that STRmix was properly applied in this case, and that I agreed with Ms. Smith's analysis that this is a three-person mixture, at least an apparent three-person mixture. One can never know exactly how many people are in a mixture from case work, but it is the most sensible interpretation that this is a three-person mixture and I agree with that.

And so I felt that the report, looking at the diagnostics from the outputs of STRmix, I agreed with the conclusion of the Michigan State Police.

Q And what about your overarching conclusion regarding the use of STRmix in general to deconvolute mixtures of DNA?

A So I feel that STRmix, and not just STRmix but probabilistic genotyping software in general, will provide a better use of the data for mixtures such as the one you are looking at here.

The way that we have interpreted mixtures in the past we would simply draw a line across that mixture and that's our threshold and then we would simply exclude loci. We would mark out loci that had data below that stochastic threshold. And so I feel that the probabilistic genotyping methods -- you know, I am really familiar with STRmix, but I have used other programs, too, that these programs make better use of the data. They are reliable and -- when properly applied.

Q So just to unpack what you -- part of your answer there,

you referred to a stochastic threshold, right?

A That's right.

Q And are you familiar with the term analytical threshold?

A Yes.

Q Are those two different thresholds?

A Those are two different thresholds. So the --

Q How does STRmix operate vis-a-vis both of those thresholds?

A Absolutely. So the first threshold, the analytical threshold is a threshold that helps the lab to determine what is signal, what is true signal versus noise.

So if you look at the electropherogram you can notice down in the very low levels down around 10 to 20 RFU's there is a little bit of bouncing up and down of what looks like maybe could be peaks. So the analytical threshold is used to distinguish if a peak is real, that is, if it's crossed this threshold it's considered to be authentic. That it's not an artifact.

THE COURT: Are we talking about -- and understand I am not a scientist. The peaks are the alleles, is that right or not?

THE WITNESS: A peak, yes, can be considered an allele if it goes across that analytical threshold.

THE COURT: Okay. And it is the alleles that identify the individual or that are in -- attributable to an individual, is that right?

THE WITNESS: I would say yes sort of. Alleles are simply just peaks. When you are trying to identify an individual you are actually looking at a genotype, which is a combination of alleles. So for example, say at a locus like THO1 is a marker that we talk about, I may be a 6/9.3. That means one of my chromosomes has six repeats. The other chromosome has 9.3 repeats. That combination of alleles make up my genotyping.

THE COURT: And these are unique to you?

THE WITNESS: No. No. That could be found in many people in the population. Because if you pick a hundred people in a room you may find several that have the 6/9.3, but when you look at all of the markers, when you look at all 20 of the markers that we test, now you are getting to the point of being unique, that combination of alleles that a person has.

THE COURT: Okay. I'd like to go back just a minute. There was at one point you talked about a threshold that would exclude loci?

THE WITNESS: Yes, ma'am.

THE COURT: Would a seven percent contributor to a mixture be in that category --

THE WITNESS: Well, so --

THE COURT: -- without this probabilistic genotyping?

THE WITNESS: So that's my key point. That's the point I was just going to make. Without probabilistic

genotyping, again, depending on the height of those peaks, if those peaks are below the stochastic threshold from that seven percent contributor, the way that we used to interpret mixtures using this approach called CPI, the combined probability of inclusion, you would exclude those from the statistic. So they could be used for interpretation but not for statistics.

THE COURT: Okay. Break that out for me.

THE WITNESS: Okay. So I have the stochastic threshold.

THE COURT: And tell us what that is.

THE WITNESS: Okay. So maybe it would be -- if you don't mind I'll just take one second to finish up on the analytical?

THE COURT: Sure.

THE WITNESS: That analytical threshold, again, is the threshold where the lab has determined any peak that falls below this analytical threshold is unreliable.

BY MR. PRESANT:

Q If I can interrupt you, under the old method of interpretation CPI or under single course interpretation or using STRmix no one is looking below the analytical threshold, is that correct?

A Well, it's possible to look below the analytical threshold if you are trying to determine things like number of contributors, but as far as using that data, no. Not for

statistics, not for inclusions, exclusions. That's -- some labs, and not all labs, but some labs may look below the analytical to try to determine if there is potentially another contributor there.

Q But for the purposes of interpretation of coming up with a statistic, neither STRmix nor previous methods used the data below the analytical?

A That's correct, yes.

Q What about the data in between the analytical threshold and the stochastic?

A Yes. This is getting to Judge Neff's question. If you have a peak that gets above that analytical, we consider it to be real. It's authentic. It is a true peak. However, there is uncertainty if that peak is below our stochastic threshold. And what I mean by that is the stochastic threshold is a threshold that the lab determines from their validation studies and that is the point at which a dropout is possible.

So you may have two alleles. Remember, I said I may have a 6/9.3, but if I am at low level, you may see my 6 but my 9.3 may be missing. So it's at that level that that level where the 6 is there but the 9.3 is missing is where I would establish my stochastic threshold.

THE COURT: Well, is that a subjective decision made by the lab itself when it is doing its validation studies?

THE WITNESS: It's made -- it's based upon the data.

It's data driven. It's not a subjective pulling a number out of the hat. They look at their validation samples. They do a lot of samples that are low level, and these are samples that are known. So we know the genotype of the sample and we are looking at the point where we start to see data dropping out or missing in the profile, and that is where that line would be drawn as your stochastic threshold. So it's based upon the data. It's not truly subjective. It's data driven.

THE COURT: Well, again, if I understand correctly, when a lab is validating the software it uses a number of known samples and that will vary from lab to lab the stochastic level or whatever it is, threshold?

THE WITNESS: Threshold.

THE COURT: I'm sorry. Will vary from lab to lab. Is that fair to say?

THE WITNESS: Well, so let's move a little bit away from what -- so in the past what labs would do, even the Michigan State Police lab, is they had the stochastic threshold, and if a peak was below that stochastic threshold that meant potentially there is uncertainty. We are not sure if this is someone who is a 6/6. So in other words, I got a 6 from my mom a 6 from my dad. I have two sixes sitting on top of one another. That one peak is 6. But if one of the sixes has dropped out, it may now be below the stochastic, so I am unsure is it really a 6/6 or is it a 6/9.3 or a 6/7 or a 6/10?

We are unsure if we only see one peak below the stochastic.

What probabilistic genotyping software does is they don't use a stochastic threshold. They are looking at the peaks probabilistically, so based upon the peak height and other things that are being modeled. They will determine the possibility of dropout that way rather than using a line drawn across the profile and saying anything below here we are going to say may have dropout. The software doesn't draw that line. It basically will model the potential for having dropout at this locus.

THE COURT: And that's all done mathematically by algorithms?

THE WITNESS: Yes. So based upon the models that are used in the software.

THE COURT: Okay. Thank you.

Mr. Presant?

MR. PRESANT: Thank you, Your Honor.

BY MR. PRESANT:

Q Moving back to your report away from the issue of the thresholds, I just want to go briefly section by section. So in the first section of the report you touch on whether STRmix has been adequately tested, and would you just summarize your conclusions for the record?

A So the question is whether -- as you mentioned, whether STRmix has been adequately tested independent of testing by the

developer.

So there are two types of validation typically. There is validation that is first performed by the developer of the software. So they will develop the software and then they will do certain testing to show the power of using the software and so forth. And that's called a developmental validation.

And then when it's published or it's made available, commercially available, the lab decides to invest and buy the software there is another validation that takes place called an internal validation. And the purpose of the internal validation is to test the software using samples developed in the laboratory with the kit that they use on their instruments in their lab.

So they can't just simply rely upon what the developer has published as validation that this is ready to go. Let's start using it. They have to do their own internal validation study. And I mentioned in the report that there are 45 laboratories at the moment that have tested, validated and implemented STRmix. So they are using it in case work. And so I feel that that is power enough that has shown that STRmix has been used, tested and validated independent of the developers.

Q Do you have any concerns about the extent to which STRmix has undergone testing?

A Any concerns to the extent that it's undergone testing?

Q That would bear on whether it's reliable. Are there tests

that should have been done on STRmix that you would have liked to see?

A No. I don't think so. I think that laboratories are doing their own independent validation. A lot of laboratories would put these validations on their website so people can look at them and see. I have went to conferences where presentations are given. There is nothing that would make me concerned about the lack of testing on some component.

Q From your review of the record, are you familiar with the arguments raised by the Defendant and forensic bioinformatics regarding whether the software needs to be tested or the code reviewed independently of the development validation and internal validation?

A I am familiar with that.

Q What is your reaction to that argument?

A Well, I think that we are talking two different things. I think there may be -- so reviewing the code can be a useful thing to do, but not by a forensic scientist. The forensic scientist is in the laboratory generating case work and is now ready to use the software. So to my knowledge there have been at least -- well, not counting the errors that were discovered in STRmix, outside of those, other software programs there are at least three or four errors that I know of. And to this date I know of no errors that have been caught by reviewing the code. They have all been caught by testing the software.

So I guess reviewing the code is a nice, I think, academic exercise, but I don't think it's quite useful for wanting to use the code in the forensic lab.

Q Now, when you say three or four errors have been caught, those are errors in STRmix specifically or other types of software?

A Oh, so I mention in my report, and it's in the section three about error rate, and I put an example of a table from a publication that we published where we were able to see an error that was in one of the software programs that was used here, EuroForMix. And the way we have caught this is that the statistic that the software gave was actually higher than you expect from a single source, from a single individual. You would get the maximum statistic if you look at all 20 of those loci. This software was giving a number that was higher than that. So obviously there was some error. There was some bug in the software, and so we pointed this out and they found the bug and they made the correction. And so we put the version 1.1 -- 1.10.0 which gave the error, and then when corrected versions 1.11.4 was -- again fell below that maximum likelihood ratio that I would expect from a single source.

THE COURT: Just, Dr. Coble, the testing that is done by labs -- and they are all, if I understand correctly, law enforcement related labs like the Michigan State Police labs. So they have got this shiny new tool to use in their law

enforcement activities. And they are testing it. They have scientists who have presumably been trained by the STRmix developers and so forth. But are there any studies that you know of, validation studies of this software which don't have any -- that are purely scientific, that purely want to find out, does this stuff work or does it not? And I am not suggesting that law enforcement labs are not properly trained. I am not suggesting that they have a result they want to reach, but is there any completely independent, independent of the developers, independent of those who would use it in their work, any independent verification, validation of this software?

THE WITNESS: Well, so I think my own personal opinion on that is the 45 labs that are now using STRmix have undergone a validation study from my knowledge independent of the company. They may have had some guidance along the way but they are the ones that are doing the actual testing. And they are also writing their own protocols from this. So part of the -- the validation study doesn't end once you have finished running all the samples. It then becomes a matter of writing up the protocol, the standard operating procedure for using the software. It also goes to training everyone to make sure that they understand how to use the software. And I would say the great deal of that is absolutely independent of anything that ESR does. So I would say yes.

Now, if you are asking about a peer reviewed publication from an independent party who has nothing to do with ESR, STRmix, those are quite hard to get published simply for the fact that generally what happens in the forensic literature is when, say, I create a new gadget that will analyze DNA in half a second, so I would usually publish that, of course I'd like to get that out there to show the utility of this new gadget. And then, you know, maybe the entire world wants to start using this and so they would like to show that they have validated this for use. But a forensic journal would not accept 10,000 papers from around the world talking about how they validated their new gadget. That would simply overwhelm the journal. No one would want to read the journal anymore. It's just simply my validation of STRmix would be what every paper would be for the next, you know, hundred years.

So generally, the way forensic journals work is they will publish the first developmental validation paper from the developer and then they may publish one internal validation study. And that one internal validation study to my knowledge that's been published so far in a peer reviewed publication was from the FBI.

THE COURT: Well, there again, though -- I mean, and maybe I didn't make my question entirely clear. You have this validation that is done by an organization that has bought the

software and presumably has bought it because it is convinced that it will be a helpful tool in their work.

What I am interested to know is whether there is any group or organization or individual who has nothing to do either with the development of STRmix, and I realize that Dr. Buckleton with whom you have worked has published a lot, but have not worked with the developer and has no -- has not bought the software for use in its work, and is purely -- I am trying to maybe -- pure science is my question. Is there anybody who or any organization who has done pure science on STRmix without any intention of using it in work or anything?

THE WITNESS: So I would say yes, there has been some of that that has happened. And I will say that I was the person that did that work when I was at the National Institute of Standards and Technology, NIST. We were -- NIST is a branch of the department of commerce, so it's a federal lab that, again, main focus is on setting standards and investigating new technology, developing new technologies.

I did testing of STRmix, TrueAllele, LabRetriever, multiple software programs. We are -- we were not a crime lab, so this is no vested interest in any program in particular. We were just simply exploring the capabilities. And I provided several public -- not publications, but presentations.

The problem as far as publishing that work, I -- at the time at NIST there was some sensitivity about publishing

that work because it started to become a -- it started to be used in the wrong way. In other words, developer No. 1 at a conference would stand up and say, see, my software is better and start using it in marketing, and that's not what NIST is about. It's not about doing a consumer report, which is what some in the community were wanting to use it as.

So those presentations are still up on the website if people want to see the comparisons, but we decided not to really publish that because it was becoming too much of a headache and just constant trying to, you know, one group is angry because their software was not put in the best light as the others and so forth. So we kind of left it there.

There have been -- there is one paper that has been published by a group in Italy. Garofano was one of the authors on that where they looked at different software programs, again, independent of any developers on a set mixture that they developed in their lab and showed the results.

THE COURT: Do you know how to spell the name of the author?

THE WITNESS: His last name is Garofano, G-r-a-f-a-n-o(sic). It was part of the exhibit, I believe from the government, if I am not mistaken. Maybe not, because that was about a year or so ago. So it's just come out.

THE COURT: Now, NIST develops standards, is that correct?

THE WITNESS: They do. Standard reference materials.

THE COURT: And they have not published or established any standard for this software, this probabilistic genotyping software, is that right? You say in your report there are no standards yet for this software.

THE WITNESS: So NIST would develop a standard reference material which would be like a tube of DNA that the lab -- so one of the standard reference materials that NIST produced is a set of DNA samples. They are liquid DNA's that the laboratories can use. They use it in their lab on their kit to make sure they get the right result. And so at this point right now every year each laboratory in the United States has to run this reference material on their instrument and make sure that they got the right result, that NIST says you should get this result. So that's sort of an example.

Standards would not be developed by NIST. NIST is not a standards -- not a regulatory body like the FDA where they say, you have to do this, you have to do that. They are not that way. So they are -- currently there is one standards, I am trying to think of the name of it, standards board. The American Academy of Forensic Sciences has established a standard organization, an SDO, a standards development organization. And to my knowledge they do have a standard of probabilistic -- validating probabilistic genotyping software. I was actually part of the group that wrote those standards.

So to sort of put it in perspective, what NIST does do is they sponsor a group called the OSAC, the Organization of Scientific Area Committees. And the OSAC is kind of like SWGDAM, which is different, but their goal is to write standards. SWGDAM writes guidance guidelines. OSAC will write standards.

So I was part of the OSAC group that developed standards for validating probabilistic genotyping software. And I am ashamed to say that was four years ago and it's been sitting -- or I shouldn't say sitting. It's been working its way through the American Academy of Forensic Sciences standards board for the last three, three and-a-half years. Every time I ask about the status I am told, it should be soon. It should be soon. But it's still in that process.

So eventually in the next hopefully, knock on wood, few months or so there will be standards that each lab in the United States that's using probabilistic genotyping software, the auditors will have something on paper that they can go in and say, are you doing this? Are you doing? Are you doing? And if you are not you could get dinged. You could get a finding for not following the standards.

THE COURT: Thank you.

Mr. Presant?

MR. PRESANT: Thank you, Your Honor.

BY MR. PRESANT:

Q Dr. Coble, you covered a number of topics there that I'd like to get to, so let's start with peer review. You note in your report that there are more than 50 articles in peer reviewed journals looking at STRmix, right?
A That's right.
Q Would you expect to see or would you like to see even more peer reviewed materials looking at STRmix?
A I certainly think it would help. I mean, obviously everything that can be published would be helpful for the community, and I think that we are starting to see -- I mentioned in my report that you have to remember we are still fairly early in this process. The first lab that I know of that started using STRmix was the U.S. army crime lab. They, I think, started using it in late 2013. Maybe 2014. So it's taken this much time to get 50 labs, I should say 50 laboratory systems up to this point. I think we are probably at a halfway point at this -- where we are at the moment with labs that are using probabilistic genotyping in the U.S. So certainly more publications would be, of course, welcomed. Not just from STRmix but from other programs, too.
Q Do 50 peer reviewed articles give you confidence that STRmix is reliable?
A I think that it shows the transparency of the models that are being used. So not all of those 50 are specifically about STRmix itself, the program itself, but may talk about some

aspect like how we model stutter, how we model, you know, peak height variability, how we model -- so there are certain aspects about STRmix that are in those publications, too.

Q Can we bring up government Exhibit 37, please? It's in one of those binders in front of you, but we'll also bring it up on the screen. And if we can go to -- let's start with this first page of the exhibit. Do you recognize this document, Dr. Coble?

A Yes. This paper just came out this year in FSI Genetics.

Q And the title of the paper is what?

A STRmix put to the test, 300,000 non-contributor profiles compared to four contributor DNA mixtures and the impact of replicates.

Q There are five authors listed there, right?

A Yes.

Q And it was accepted on March 20, 2019?

A That's right.

Q Can we go to the next page, please, and scroll down? Do you see where it says declarations of interest?

A Yes.

Q What's the purpose of a declaration of interests section in a paper?

A So this is something that journals have been adding in the last few years just wanting the readers to realize if there is any conflict of interest. So this has been especially a

problem in the clinical world where a clinical study may be funded by a pharmaceutical company and they don't let the reader know that. But in this particular case there is no -- nothing to declare as far as a conflict with any part of this study.

THE COURT: Are you familiar with any of those authors, Dr. Coble?

THE WITNESS: I do know Sara, and I do know Diane quite well. Have met them at conferences and have had some e-mail correspondence with them in the past.

THE COURT: And what is their -- who are they and what do they do?

THE WITNESS: So this is a laboratory in Montreal in Canada. And I first was sort of got to know them because they were doing -- when I was at NIST I did this interlaboratory study where I took set mixtures, these were mixtures that I had made, and sent them out to labs to analyze and then give me their work back and sort of see how we are -- how are we doing. And so in conversations with Diane, who I think is the technical leader of their laboratory, they were actually doing their own sort of interlab studies. They were actually creating their own mixtures and testing the people that are working in the lab to see how well everyone was on the same page when it comes to interpretation. So yes, they are a laboratory that's in Montreal.

THE COURT: Thank you.

BY MR. PRESANT:

Q Would you scroll down a little bit, please, Dr. Coble? Dr. Coble, I am not going to take the time to go through all 26 pages of this particular paper, but would you just discuss or read into the record the highlights that are noted here on the first page?

A So the highlights, they state that they created these complex known, and that's a key word. So in this case they know the people that are in the mixture, and they created four-person mixtures or what looks like a four-person mixture. And these mixtures had minor contributors. And then they compared the results. So they ran these through STRmix and then they compared the results to 300,000 people that they know are not in the mixture. And so you expect, based upon the behavior of the likelihood ratio, that people who are not in the mixture should give a likelihood ratio less than one. And that's what they found in 99.1 percent of these non-contributors gave the correct likelihood ratio, less than one.

When they used replicates, in other words, they took this four-person mixture and they replicated this, they amplified it, you know, multiple times. And when you use two replicates or so -- whenever you use two of these samples then they noticed that you got higher specificity. So in other

words, 99.8 percent of the time the likelihood ratio was less than one when you used a replicate amplification.

MR. PRESANT: Your Honor, government moves to admit Exhibit 37?

THE COURT: Ms. Kloet?

MS. KLOET: No objection.

THE COURT: It's admitted.

BY MR. PRESANT:

Q Let's turn to 38, please. Do you recognize 38?

A Yes. Your Honor, this is the paper I was referring to. I misspelled his last name. The last author is Paulo Garofano, G-a-r-o-f-a-n-o. And this is a group from Italy. So you can see their affiliation, and none of these authors are associated with STRmix.

Q Can we go to page 7 of the PDF, page 149 of the publication, and scroll down to the section that says, conflict of interest statement? Do you see that section there, Dr. Coble?

A Yes, sir. So the conflict of interest, the authors of this manuscript certify that they have no affiliation with or involvement in any organization or entity with any financial interest or nonfinancial interest in the subject matter or materials discussed in this manuscript.

Q You are familiar with this paper from before today's proceeding?

A Yes.

Q Could you summarize for the Court the principal conclusions of the authors of this paper specifically with respect to STRmix?

A So one thing that I thought was quite interesting about this paper, and it might help the Court if we move up to probably page 3. I'm sorry. Let's go down. Okay. Right here.

Now, the interesting thing about this paper is that they used one of those tubes of DNA that I mentioned that NIST provides. And NIST provides these samples of DNA. So they actually used some of this DNA from NIST to create their mixtures. So these are known individuals. So we know their profiles. They created the mixtures.

And so let's just take a look at the, on the right hand side. They are looking at five different software programs. Along the top in the diamond is STRmix. The orange square is EuroForMix, and the purple triangle is DNA-VIEW. These three software programs are what we call continuous probabilistic genotyping programs. There are two different types of probabilistic software. There is continuous and semi-continuous.

It's probably easier to explain the semi-continuous first. The semi-continuous software simply look at what peaks are there, what alleles are there. They don't look at the

height of the peak because the people that advocate this type of software believe when you get very low level samples, peak heights don't behave the same way when you are at high amounts of DNA. If I am at high amounts of DNA and I have two peaks, they should be very nicely balanced. But when I have low levels of DNA you may see things like this, where the peak heights are way imbalanced.

THE COURT: And are we talking there about where you just have trace amounts?

THE WITNESS: Yes. So generally when you have a very low level you may get this really extreme imbalance. And to be quite honest the most extreme imbalance you would have is one peak is there, the other peak is gone. So there is nothing really to compare to because the sister allele has dropped out.

THE COURT: Does that mean, then, that the results are not reliable or not conclusive? What does that mean?

THE WITNESS: Not necessarily. So it depends upon the modeling that's done, because what the probabilistic programs will do is that they will either directly or indirectly will model or account for dropping out the probability that you may have missing data. When you are at this low level there is a higher probability that you are going to have missing data than when you are at high levels of DNA. So it will model that and take that into account and adjust the likelihood ratio depending upon the modeling that's performed.

THE COURT: Does it tell you how much missing data there might be?

THE WITNESS: Well, this is, again, a difference between the two different software approaches. The semi-continuous, the analyst has to first go through and estimate or guess what is that probability that I may have missing data? So that could be a subjective thing. You know, it's based upon what peaks they can see that are at low level. Based upon the peak height they may use some kind of a curve to figure out, okay, when I am at this level the probability of dropout is 70 percent of the time. So they would use that number as part of their calculation.

The fully continuous software programs like STRmix and EuroForMix and DNA-VIEW, they don't do that. They do -- they will model whether dropout is possible based upon the peak heights that are there. So they will use the peak heights and then they will model whether dropout is possible. So when you have a very low level peak, there is a pretty good chance that there is dropout there and it's going to model that as part of the process.

So the thing to notice first that I thought was really interesting about this paper and really makes sense based upon what I have seen, too, in the past, is notice that this is a three-person mixture here on the right-hand side. We have got a ratio of 20:9:1. So that's, you know, quite a low level,

20:9:1.

BY MR. PRESANT:

Q So the minor contributor there is about three or four percent?

A That's right.

Q And then 8:1:1, 6:3:1, and 1:1:1.

Notice the likelihood ratio for both -- or for STRmix, EuroForMix and DNA-VIEW. They are all almost sitting on top of one another. These are three different programs, three different modeling approaches, and they are all reaching the same conclusion, that the likelihood ratio is somewhere between 10:20th to 10:23rd or 24th.

So I felt this was interesting because here again it shows that when you are using all of the information that's what a continuous program will do. It will use the peak heights. It will also model things like stutter. It will model things like dropout and things like that when you are modeling these factors. Then notice we are getting pretty much the same result.

It's also interesting to note the semi-continuous programs, the red X LRmix Studio, and the green plus sign for LabRetriever, notice your statistic is pretty much the same thing. Again, different models are getting the same result in this particular example.

MR. PRESANT: Your Honor, the government moves Exhibit

38?

MS. KLOET: No objection.

THE COURT: Submitted.

BY MR. PRESANT:

Q Dr. Coble, you touched briefly on the error rate standard section of your report already, but would you summarize generally what we should consider to be the error rate for STRmix?

A Well, I think this is somewhat a difficult thing to really quantify. Historically, I think, at least in the last few years, a lot of people are looking at these false-positive and false-negative. So just like the previous paper that we talk about from Montreal where they use 300,000 people that they know are not in the mixture to see what kind of likelihood ratio they get. Greater than 99.1 percent of the time the likelihood ratio was less than one and probably zero. A small percentage of the time you may get a likelihood ratio that's greater than one. And I don't know exactly what that was in this particular paper. I haven't really looked at it that close in detail yet. But they would consider that when you have someone who is not in the mixture that gives you a likelihood ratio of greater than one to be a false-positive. Whereas a false-negative would be someone who is actually in the mixture but they give you a likelihood ratio that's less than one. So that's a false-negative. They should have given

you something greater than one but they are giving you something, a statistic that's less than one, likelihood ratio less than one. I don't really think those are considered errors in my opinion.

Q Why not?

A Well, so if I were to create 300,000 people and let's say I have a low level mixture, then there is a chance just by chance that I would create a person that would actually look like they have contributed to the mixture. And in that case you would get a likelihood ratio that's greater than one. It may not be huge. It may be ten. It may be a hundred. But what that's saying is not that the soft -- it's not saying that the software did something wrong. In fact, I would say the software got it right. If I were to give the software a profile that looks like it should be there, and I get something greater than one, I would say the software was correct. I would not call that an error, in my opinion, because I just so happened to create out of the wind here, out of the blue a profile that would match this potential contributor.

So what Alan Turing, and this was mentioned in the testimony from last year, what Alan Touring developed back during World War II -- he was, of course, part of that group in Bletchley Park that was working on the breaking of the Nazi code. And he was asked what's the error of a likelihood ratio? And he said it's about one over the likelihood ratio that you

would expect. One in 300,000 times you would have a likelihood ratio that's greater than one or greater than whatever likelihood ratio you would get.

So when I think about errors, I think about things like I said in this report where you catch that because you are running samples that you know and you see where maybe there was an error that way. And again, I reiterate, I have never heard of anyone catching an error by looking at the code. It's usually done by testing.

The other thing that I would like to point out is, and based upon what I have looked at in the Michigan State Police protocols which we mentioned was the big thing that you do once you finish your validation study is you write up your procedures, your protocol, is that the software is not being used as a black box. It's not a magic eight ball where we shake it up and we look to see what number we get. There is another level of interrogation that the analyst will do, and this is in the Michigan State Police protocol. I noticed the checking the diagnostics.

There is also an interpretation that the Michigan State Police will do as to whether or not a sample should even go into STRmix to begin with if it's too complex. If it looks like it's a six-person mixture we are not going to put it in the software.

THE COURT: How is that determined?

THE WITNESS: Well, many laboratories will determine the number of contributors based upon a couple of things. Some laboratories look at the maximum allele count. So if you have two alleles at THO and I have two alleles at THO and we mix our DNA together, you would expect to see four. And if you see no more than four alleles that's an indication of a two-person mixture. If we add another person into the mixture we now expect to see no more than six alleles. And we add yet another person into the mixture we now expect to see no more than eight alleles. Well, if you see nine alleles that means you probably have more than a four-person mixture. You probably have a five-person mixture. And so based upon that maximum allele count at any particular locus, some labs will also look at peak heights to maybe help them, you know, determine because sometimes you may see a mixture where there is six alleles but it's actually a four-person mixture because of the sharing that could be going on, allele sharing. They may look like it's a three but it's actually a four. So there are many different ways that laboratories can determine the number of contributors based upon mostly the maximum number of alleles at any locus and potentially peak height information to help.

THE COURT: So that part of it is not an exact science?

THE WITNESS: It's not an exact science. And again, this is also -- in my observation from talking with labs, this

is a point where the decision may be made that this mixture is too complex. If it's difficult for you to determine how many people are in the mixture, that's probably a sign that you probably shouldn't be analyzing it. That it's too complex.

THE COURT: And in this case there was -- there was a determination that it was -- there were at least three and maybe four contributors?

THE WITNESS: At least three and I guess the report was that a fourth contributor may or may not be able to be determined.

THE COURT: Okay. Thank you.

BY MR. PRESANT:

Q How confident are you, Dr. Coble, that there are three contributors in this case?

A I think based upon looking at the electropherogram I feel very confident saying this is a three-person mixture. There is obviously some degradation that's going on at the high molecular weight loci, but based upon the -- especially the lower molecular weight, if you are looking at the electropherogram, on the left-hand side of that electropherogram, it looks fairly confident to me that this is a three-person mixture.

Q Could be a four-person mixture?

A It certainly could. We never know. Again, when you are talking about case work you never know the true number of

contributors. The best we can do is estimate.

Q And that's also true with single source DNA interpretation, right?

A That's right.

Q It's possible that in traditional DNA analysis where we thought there was only one contributor there is a chance that there was actually a second contributor, right?

A If there is a lot of imbalance it looks like it's a single source. If there is a lot of imbalance and potential dropout there, yeah, it's possible. I actually have examples that I do in my training classes where I'll have, like, eight or nine different mixtures, and they are, you know, easy simple single source, and then a really complex mixture. And I have one example where it looks like a single source but it's really a two-person mixture and most people say it's a single source.

THE COURT: Sounds like the chemistry class I took in high school where you had to analyze stuff. A hundred years ago at least.

BY MR. PRESANT:

Q You need to be a trained forensic scientist in order to make those judgment calls, right?

A That's right. And I will say that a number of contributors, again, is not a unique aspect of STRmix. That's back in the interpretation stage. So when that data comes off the instrument, that's one of the first things the analyst will

do is they'll look to see are there any artifacts? Is there anything I need to account for? And how many people do I, you know, think are in this mixture? That's independent before you even put it into STRmix as you sort of get an idea on number of contributors. It's not a, you know, problem to STRmix.

Q Has anyone studied, to your knowledge, the effect on the likelihood ratio from the misinterpretation of the number of contributors?

A So there have been some publications. I can't -- let's see. I am trying to think. Oh, yeah. So Duncan Taylor, who is one of the architects of STRmix, he published a classic paper on basically validating STRmix where he took a set of mixtures that were -- you know, they were really three-person mixtures but he ran it as if it were a four-person mixture or if it was really a four-person mixture he ran it as a three-person mixture. So running it through the software if it were really a three but you run it as a four and it's really a three and you run it as a two to see what the behavior of the likelihood ratio is if you have one extra or one less contributor to the mixture.

THE COURT: So when you run it you tell the software how many people you think were in it?

THE WITNESS: That's right. At least this version of the software that the Michigan State Police are using you have to tell the software how many people are in the mixture. The

newest version or the current version of STRmix has the ability for you to click a button to -- where it will, say, vary that number plus and minus one. So in other words, if I think there are three people do it as a two and do it as a four and do it automatically. You don't have to set it up. And it will do that in both the numerator and the denominator. So it will vary the number of contributors and it will provide you what's the maximum likelihood ratio.

BY MR. PRESANT:

Q What's the effect on the likelihood ratio from accidentally having one fewer contributor than there were, in fact, in the mixture?

A So typically what will happen if it's really truly a three-person mixture but you say it's a four, it typically won't have a lot of effect on the likelihood ratio, especially for the major contributor.

Q I was actually asking you the opposite question. I got the wording wrong. That's say it's actually a four-person mixture but it's misinterpreted as a three?

A Right. So typically there is very little harm in running a four as a three. I would say that, let me just say if I can it helps me to get this straight. If it's a three but I run it as a four it's going to have to create a fourth contributor. So it's really a three but I am saying it's a four, so it's going to have to create a fourth contributor. So it will use a

little bit of a peak height from other contributors in there to create that fourth person. Usually that likelihood ratio is close to one because it's really someone who is not there. So when you interrogate it will potentially lower the likelihood ratio for the other contributors.

Q To the people that are actually there?

A That are actually there. So the true contributors the likelihood ratio may get lowered a little. Probably not for the major contributor. Probably still going to stay the same if it's like a 60, 70 percent contributor. Probably going to have zero effect on the likelihood ratio for a major contributor. For the minor contributor of a three-person mixture you run it as a four there may be a slight lowering of the likelihood ratio. It just really depends on the mixture itself.

THE COURT: Is there a point at which it is considered to be unreliable, for instance, if you had a -- the software come back and say that the third contributor was two percent, would you consider that to be reliable?

THE WITNESS: Well, I think based upon if I had a contributor that was two percent and I am just going on what I would expect, again, not having actual, you know, an example in front of me, but what I would expect to see is a two percent contributor would probably give me a likelihood ratio that's close to one. That's -- since it's so low level, remember we

talked about when you have really low level peaks there is a lot of that modeling of dropout that's going on and that creates uncertainty in STRmix and that's going to be reflected in the likelihood ratio. You are going to get likelihood ratios that are about one. And so I don't know if I would call that unreliable, but I would call it definitely uninformative.

THE COURT: At what level?

THE WITNESS: Well, I don't -- I don't know that you can pick a certain percentage, because, say, like, five percent. I know that this was a thing that the PCAST report initially said 30 percent was, you know, that was it.

MR. PRESANT: Twenty percent?

THE WITNESS: And then they said 20 percent. The first report was 30 percent. Then they dropped it down to 20 percent. I don't know where they got those numbers from. I think they maybe did some magic eight ball or something. But I have seen samples that are reliable down to, you know, five -- four and five percent.

Now, these are, of course, mixtures that I have made and you know, so I know the contributors and so forth. And so I kind of have the -- but I think it's hard to say that, well, when you've got this percent contributor, then yes, it's -- that's it. I mean, if it's one percent, two percent I think you are going to get likelihood ratios less -- at/or less than one.

BY MR. PRESANT:

Q So another way of saying that is the less DNA you have the harder it is to interpret the end result, the likelihood ratio is going to tell you that that data was too hard to interpret?

A That's right. The less information you have the more uncertainty you have and that would be reflected in the likelihood ratio being close to one.

Q While we are still on the issue of the number of contributors, can we bring up government Exhibit 4 previously admitted? And let's just scroll to the title and authors. Do you recognize this paper, Dr. Coble?

A I do.

Q What is it?

A So this was a paper that was a multilab publication in response to the PCAST report. There were, I think, about -- yeah, there were 31 laboratories that provided their internal validation studies and -- in this particular paper. And this is a compilation of that study.

Q Can we go to page 18, please? Do you see the section here, Dr. Coble, that describes likelihood ratios under the assumption of N and N plus one contributors?

A Yes.

Q Is that the same issue we were just discussing where the assumption of the number of contributors was incorrect?

A That's right. Where you would have, say, for example three

and four contributors.

Q And let's look at the figures. Can you help us interpret what's being depicted in these figures?

A So in -- what we are looking at is a plot where they take the sample and test a three-person mixture on the bottom, a three-person mixture that's treated as a three. So this is a known three-person mixture. And we ran it through the software saying this is a three-person mixture.

Along the Y axis, on the left-hand side, we are looking at the three-person mixture but we ran it as a four-person mixture.

Q That's right here?

A That's right. Now, a straight line that's drawn here diagonally will say that the likelihood ratio you get when you run this three-person mixture as a three, if it gives you the exact same likelihood ratio as this three-person mixture run as a four, then it will fall on that line. That line means they are equal to one another. So if I were to -- I don't know if you could at the bottom see where it says 10, and draw a straight line up to the curve, or I'm sorry, straight line up to the diagonal.

Q You can actually draw a line just by touching the screen with your finger.

A And here is 10. So at this point where they meet they are both giving you a likelihood ratio of 10 whether you run it as

a three or you run it as a four. And what I would like to point out here is that most of this data is falling below this line. So in other words, if -- and I'm sorry, could you clean that? I do have a way to clean that?

Okay. If the mixture was really a three-person mixture and you ran it as a four-person mixture, so I am going to go here and I am going to go across -- didn't mean to -- let's do this one. Here and here. What this is saying is that if you ran this mixture as a three-person mixture, it really is a three-person mixture, you are going to get a likelihood ratio of about 10 to the, let's say, 22. But if you ran it as a four-person mixture you are going to get that likelihood ratio of about we'll say 17. So here is the effect of not getting the -- of saying that there is more people there than it should be is the likelihood ratio is lower.

Q In other words, less favorable to the prosecution?

A That's right. More favorable to the Defendant in this case or the person of interest. I'm sorry. Five orders of magnitude less than if you ran it correctly as a three-person mixture than if you ran it as a four.

We get the similar kind of result over here on the right. This is, again, running a four-person mixture as a four versus running a four-person mixture as a five. You can see that most of the data is falling below that curve which means you tend to get lower likelihood ratios in favor of the

prosecution hypothesis when you run this sample with one extra contributor.

Q Can we go to the next page, please? What do these figures on the next page show?

A So it's a little difficult maybe to see, but what this --

Q Can we zoom in?

A What this curve is showing here, this is a three-person mixture analyzed as a four is the dark line here. And the dash line here is a three-person mixture analyzed as a three. And so what this is looking at -- and again, I think this is maybe a non-contributor test. I can't really see based upon the figure description. But the dark line is saying this is a three-person mixture analyzed as a four. And I think this is looking at either the minor contributor or maybe non-contributors. It's kind of hard to tell at the moment without having the paper, but you can see that most of the likelihood ratios when you run a three-person mixture analyzed as a four for, I think this is for non-contributors, give you likelihood ratios. And here is -- I know it says zero, but this is on a log scale so a log of zero is one. So most of the data is at one or less. The bulk of it is. So you can see here on the left-hand side the density, so about 80 percent or about yeah, 80 percent or so of the curve here is less than one.

Q Well, let's go to words. If we can scroll?

THE COURT: Let's not spend a lot of time on these graphs, okay, Mr. Presant? You have said you had just a few questions and we are really getting into it. So could you get a little more towards the heart of, again, what I requested Dr. Coble and Dr. Krane to answer?

MR. PRESANT: Yes, Your Honor. And I was just trying to address the issues with respect to the number of contributors.

BY MR. PRESANT:

Q So if we go past the graphs to the bottom of the page we get to the bottom line wording where it says the conclusion of the paper is what with respect to the number of contributors?

A So the general result was a decrease in the likelihood ratio for true contributors after the assumption of an additional contributor to the mixture.

THE COURT: We are talking about, Exhibit 4 here?

MR. PRESANT: Yes, Your Honor.

THE COURT: Thank you.

BY MR. PRESANT:

Q So let's go back to your report. The next section we were on was the maintenance of standards and certifications and the extent of validation by Michigan State Police. That's page 5 of your report.

A Okay.

Q A little higher up, Ms. Norton.

A So again, looking at the government Exhibit No. 10, which was the validation summary of their STRmix validation, I find that -- I found that they followed the SWGDAM guidelines for validating probabilistic genotyping software, and so I felt that this is consistent with other internal validations and publications that I have observed in my work with the forensic community, even the work that we are doing at the University of North Texas. We are currently validating STRmix and we are using the SWGDAM recommendations.

Q You testified earlier about SWGDAM setting guidelines and OSAC setting standards for probabilistic genotyping software, right?

A Yes.

Q What's your opinion on whether the STRmix version at issue here, 2.3.07, complies with SWGDAM's guidelines?

A Yes. I think that it does. They follow exactly the types of experiments that SWGDAM has recommended to do, the adding one contributor more than there really is there, doing less than one, you know, doing the different variations in the testing that you are doing during your validation study. So it seems to me that they are following the SWGDAM guidelines.

Q And what about OSAC's proposed standards? Is STRmix generally, and the work done by the Michigan State Police here, going to be in compliance with OSAC whenever those guidelines or standards come out?

A Yes. Again, I am not part of that standards development board that's working on the standards that will be made available in the near future, but I can tell you that what we sent to them as our recommendations for standards were derived from the SWGDAM guidelines. So unless something has drastically changed, and I wouldn't think that it has, I think that -- that all labs will be in compliance with the standards once they are made available if they have followed the SWGDAM guidelines.

Q Now, the Court also put to you the question of external auditing of the Michigan State Police's validation work, correct?

A That's right.

Q And you said that you couldn't find information in the record, right? This is on --

A Yes. Yes. That's right. So usually unless you have that audit document where the auditor will say you have brought on in this year, you know, STRmix or you know, GeneMapper, unless you have that document it was tough for me to say, but generally you would get an eyes, a pair of eyes or maybe more than one pair of eyes that are looking at validation studies of STRmix from your external auditor during your audit.

Q You would expect the Michigan State Police to have done that?

A Yes.

Q Can we bring up government Exhibit 33? These are lengthy documents. You may want to look at them.

THE COURT: Are you going to admit Exhibit 4?

MR. PRESANT: 4 was already admitted, Your Honor, at last year's hearing.

THE COURT: Oh, sorry. Thank you.

BY MR. PRESANT:

Q You may want to look at them, Dr. Coble, in the bottom of your file.

A Okay. I'm sorry. Did you say?

Q 33 we are going to start with.

A 33. Okay. Okay.

Q And have you seen 33 before or documents like 33?

A I have seen documents like 33. Yes.

Q And what is this document generally, this type of document?

A So this is just the result of the audit for, in this particular example, the Michigan State Police conducted by the external reviewers here, Paul Bush and other colleagues here. I think if I am not mistaken Paul is from Iowa. So -- and this is the typical type of audit process that an external auditor in this case would go through. These are the quality assurance standards that were developed by the FBI. And so when the laboratory gets audited these standards are looked at.

So they will come in. They will do a review. They will actually do interviews with people and things like that

during this process. And so this is the output. They go through and check the box yes they do comply or no they did not comply with this particular standard.

Q Can we go to the last page of the document, page 97? I'm sorry, page 99 of the PDF?

A Okay.

Q It says 97 at the very bottom of the PDF?

A Yes.

Q But I guess the way the exhibit is set up it's 99. So what are we looking at here in appendix E of this document?

A So appendix E is this -- this is documenting any proved validations according to standard eight. And so to be completed is the list of validations, PowerPlex Y, which is a Y STR testing kit on the 3130. That's an instrument that's used to generate the data, validation verification of PowerPlex Y on the 3500 series of the genetic analyzer, validation of PowerPlex Fusion, which is an STR kit on the 3500 with GeneMapper ID-X software that analyzes the data and then performance verification of Y screening of sexual assault kits.

Q So these genetic analyzer validation protocols are four procedures and processes that the lab would use to produce the electropherogram that might eventually go onto STRmix, correct?

A The data, yes.

Q The data?

A Yes.

THE COURT: But not -- I just want to make sure the record is clear. This does not speak directly to the validation process of STRmix by the Michigan State Police, is that correct or not?

MR. PRESANT: We are going to get there, Your Honor.

THE WITNESS: Yeah. Not right now.

THE COURT: But not this document?

THE WITNESS: All this document says is that the audit team has reviewed the validation studies that were performed. There were actually four: PowerPlex Y on the 3130, PowerPlex Y 23 on the 3500, Fusion, which is the STR kit that's used for case work for criminal -- the Y kits are for male. The Fusion kit is used to generate these STR's that we are talking about putting in the STRmix, and then Y screening of sexual assault kits.

THE COURT: Okay.

BY MR. PRESANT:

Q Can we go to page 93 of the PDF? It's marked as page 91 of the document. Now -- I am sorry. It's appendix A. So maybe it's page 91. I am not sure what happened there with the numbering. What is this appendix A, Dr. Coble?

A So appendix A is the findings and responses. So when a lab gets audited the external auditors again will come in. They will pull some random cases to look at. They will look at the validations that were performed in the last term since the last

audit. Again, they will interview analysts and things like that. So they'll do this sort of inspection if you will. And if they find something that is out of sync, something that where the lab is not following a standard, that's called a finding. And so here in appendix A the auditors have said there is no findings. So they found nothing out of order. It looks like the lab is following procedures correctly and there is nothing to be concerned with. If there was a finding the laboratory has the chance to respond to, you know, potentially with corrective actions that will be undertaken and so forth.

Q Can we go to Exhibit 34, please? What's 34, Dr. Coble?

A So 34 is, again, another audit that was performed. This time this is covering from -- in October of 2016 to November of 2016 over the period that the audit was conducted.

Q Can we go to the last page of this document, please?

A So again, on the last page this is appendix E. And again, these are validations that the auditors reviewed when they did their audit. And the list of validations include STRmix software validation. The validation was conducted collaboratively between Lansing, Northville and Grand Rapids. And the other thing is material modification for the PowerPlex Fusion stochastic threshold.

Q So this external audit would cover STRmix that was used by the Michigan State Police in this case?

A That's right.

Q Can we go to appendix A, please, which is page 93 on the document, page 95 of this PDF? What is appendix A?

A So once again, appendix A is the summary of findings and responses. In this case in this audit the findings is that there are no findings or non-conformances.

Q Can we go to Exhibit 35, please? Do you recognize 35?

A Yes. So this is -- Exhibit 35 is a certificate from the American Society of Crime Lab Directors, the laboratory accreditation boards. We call that ASCLD lab. And they have declared here that the Michigan State Police Forensic Science Division, Lansing Forensic Laboratory, has met the requirements of -- you know, for the standards that are -- were examined and so they have received the accreditation for ASCLD lab international for forensic science testing.

THE COURT: This is a general, you are doing everything right kind of thing?

THE WITNESS: Yes. So this is just to assure that we have an external group of scientists have come into the lab. They have been given access to case work. They have looked at our validations that we have done, and they have interviewed people and so forth, and so they have approved that they are in compliance.

BY MR. PRESANT:

Q Let's go to Exhibit 36, please. Do you recognize 36?

A 36 is a letter from Dr. Doug Hares. He is the NDIS

custodian. He is basically the person who is in charge of our national DNA database, and he is with the FBI CODIS unit. And this is a letter from Dr. Hares to Kristen Schelling from the Michigan State Police, and this is just to say that in response to your audit --

THE COURT: I really don't think we need all of this, Mr. Presant. I mean, I get it. This is the kind of thing that somebody is saying they are doing it all right. I get it.

MR. PRESANT: And Your Honor, the Court raised the concern of external auditing. I want to do my job as the government's lawyer.

THE COURT: And you have done it very well. Thank you.

MR. PRESANT: Then, Your Honor, I'll move to admit 33 through 36, please?

MS. KLOET: I have no objection.

THE COURT: They are admitted.

BY MR. PRESANT:

Q Okay. Dr. Coble, let's look at government Exhibit 40 then.

A I'm sorry?

Q 40.

A 40.

Q And do you recognize this document?

A I did actually receive this document on Friday, I think, and I did get a chance to look over it, yes.

Q And what do you understand this document to be?
A So this is what looks to me to be a letter from the DNA technical leader for the Michigan State Police. And this is basically giving some additional information about the internal validation of STRmix, and specifically the type of samples that were run at very low levels.
Q And you understand -- well, have you reviewed Dr. Krane's report in this case?
A I did, yes.
Q And did you understand one of his critiques regarding the internal validation study or his primary critique involving it?
A Yes.
Q Would you summarize what that is?
A In summary I think Dr. Krane's critique, it appeared to him that the lab did not run a number of samples that were at really low level, say seven percent or less, in order to establish is this low enough that we can say we can't have or we don't have, I guess to use your word, reliable results. I would say informative results. So I think that was the general theme of Dr. Krane's report there on that section was that didn't appear from the validation summary that this sort of information about how low we should go was included.
Q Did you understand him to be particularly pointing out that he didn't see studies that were down to both sort of low level of minor contributors and low level of actual mass of template

DNA in the same experiment?

A That's right. So it's one thing to say, like, the PCAST report why a little -- was being a little cagey about that was. They said 20 percent. Well, if I have two nanograms and 20 percent of that, that's going to give me a sufficient amount of DNA. That's going to give me reliable results. But if I only have, you know, a hundred picograms at 20 percent now I am staring to figure that I am -- the results are going to be really uncertain. So it's not just the percentage that matters. It's also how much DNA was there.

Q What's your view of that position that there should be experiments that show both the percentage of the minor contributor and the actual amount of template DNA in order for the validation study to actually capture case work that falls within those parameters?

A I agree with that. I think that's something that labs do and should do as part of their validation study.

Q If a lab only did a study down to show that it could handle samples down to, for example, four percent of a minor contributor and separately showed that they could handle down to 20 picograms of DNA, would it be a fair inference, in your opinion, that they could handle samples down to 20 picograms where the minor contributor was only four percent?

A I think you need to do both. I think you need to have the combination. The effects that you will see when you run those

types of samples through STRmix will provide you more data, more information. Again, it's developing that sort of understanding. And again, I want to also point out the fact that it's not just putting this into the software and you are getting an answer out. It's also looking at that report. It's understanding the diagnostics, understanding, does this make sense? And that's something that's really important. And I have been preaching to the community that it's completely inappropriate to just simply treat the software as a black box. You plug the data in. You let it spit out a number. You copy and paste that into your report and you are all done. There is another layer of interpretation and understanding has to occur. And I see in the protocol that the Michigan State Police do this. I know other software programs, not STRmix, where basically it's a blind cut and paste kind of thing. That there is not a lot of post-analytical interpretation, so that's concerning.

THE COURT: What does that analytical interpretation involve?

THE WITNESS: Well, it's simply looking at the diagnostics. Did the -- you know, things like the Gelman-Rubin statistic and things like that. Does it look like the software had enough time? Did it run properly? Are there certain statistics that you can get out of that report looking at the weights? So if I have -- let's say for an example I have a

mixture that is let's say 90 percent is from you, Judge Neff, and 10 percent is from me, but if STRmix says this is 50/50, that's a red flag. It doesn't matter if it gives me a likelihood ratio of a kagillion. If this says that's a 50/50 I am concerned. So that's the kind of diagnostics that you would look at in the report after it's been run and not just simply blindly accept what's going on.

THE COURT: Is that what you meant on the last page of your report where you say the diagnostics of the STRmix report are intuitive? Is that what you are referencing there?

THE WITNESS: Yes, ma'am. So looking at the weights, looking at the -- you know, if you look at that mixture you can kind of see there is a major, maybe what we would call a mid and sort of somewhere in the middle and then there is a trace, a low level. And so the percentages that the report said it was 67 percent or 60 percent, that makes sense to me based upon what I receive. If I had gotten something that was really out of bounds, you know, that would make me think and then maybe want to rerun the sample or you know, do something else. Not just simply rely upon what the software spit out but doing that sort of interpretation and understanding of what does it mean?

BY MR. PRESANT:

Q Let's go to page 3 of Exhibit 40, please. What does this table show, Dr. Coble?

A So this is showing some examples of mock, I guess mock case

work wherein this particular case they created samples like blood stain from a boxer short, the swab of a rear passenger door handle and so forth. And again, this is where you have known contributors, so we know whose blood this is on this boxer short. Say we have a three-person mixture, and in this table we are showing first the item and then the quantity. This is how much DNA was determined from this sample.

And then the next column is how much DNA was put into the PCR reaction. So in the first example 30 picograms were amplified and then as a number of contributor, three. And these are the ratios. So 76 percent, the major contributor was three-fourths of the DNA. Twenty-three percent for -- that's how many picograms you would expect from a 30 picogram sample. If 76 percent is from one person that means they contributed about 23 picograms of that 30. Fifteen percent from the second contributor and nine percent from the third contributor.

Q So in this case you understand that the minor contributor is seven percent of the sample, and the estimated amount of DNA there is 49 picograms, right?

A I am sorry --

Q Not on this table. I am saying from the -- from the case work in this case?

A Yes, sir.

Q Seven percent and 49 picograms?

A That's right.

Q So all of these green squares right here are examples from the internal validation study of the Michigan State Police where they looked at samples where the minor contributor was at least as low as seven percent and had at least as little as 49 picograms of template DNA?

A Yes, sir.

Q Let's go to the next page, please. What does this table show?

A So this is showing the mixture ratio of the lowest contributor that were performed. So here we have, for example, the first one is a ratio of 10:7.5:1. So you've got sort of a high, another kind of high and then a very, very low contributor. And here they amplified 1,000 picograms, which is also known as one nanogram. So we use our -- the quantities are a little interchangeable here. 1,000 picograms is equal to one nanogram. So this is a three-person contributor and the lowest percent contributor here was 5.4 percent in this mixture which represents 54 picograms.

Q So in this table 2 from additional data from the internal validation study you see examples where the lowest contributor is the below 7 percent and the calculated amount of DNA from that contributor is less than 49 picograms, correct?

A That's right.

Q There is one right there. 4.7 and 47. 3.2 percent and 32. And it goes down from there?

A That's right.
Q So the last part of your report, Dr. Coble, we haven't talked about this morning yet is regarding general acceptance in the community. What is your view on whether STRmix is generally accepted within the scientific community?
A I think that the real -- as we say, the proof is in the pudding. I think that the fact that we have at the moment close to 50 laboratory systems. Now, that doesn't mean just 50 labs, because some laboratory systems have multiple labs. So three here in Michigan. There are 12, I think, in Texas. There is another nine or ten in California that are using STRmix. So we are actually looking at a number of labs. Well over a hundred.
THE COURT: Well, of the three here in Michigan, wouldn't you have -- if the State Police has three labs -- I knew they had two. I didn't know they had one in Grand Rapids. But they would all work off the validation that's done at the central lab, right?
THE WITNESS: That's right. But they are using this -- so they use that validation to be able to set the parameters that are used by the software in interpreting mixtures. So -- but the case work that they are analyzing is in their labs so they are three separate labs and they are analyzing different --
THE COURT: Well, but they are accepting the

validation of the software that was done once by the central lab? I mean, they are not revalidating?

THE WITNESS: Right. So the initial validation was done -- it said in that audit document that the initial validation was conducted in collaboration with the three labs. So this is accepted SWGDAM -- I think in the SWGDAM validation, just validation document, not probabilistic validation, says that if you have a multiple lab system, if you show that the instruments in the multiple labs are all sort of behaving in the same way within a certain sort of, you know, combined results, or you know, very similar, then you can do one validation to satisfy all of the different laboratories.

MR. PRESANT: Before I come back to that I jumped ahead. Your Honor, I wanted to move Exhibit 40?

MS. KLOET: Yes, Your Honor. I object on authentication and hearsay grounds.

THE COURT: That was the letter from the State Police technical leader?

MR. PRESANT: Correct, Your Honor. And the government has people here from the Michigan State Police today if the Court wants to hear from them directly to satisfy the foundational issues.

THE COURT: Let's hold off on that for a minute.

MR. PRESANT: Very well.

BY MR. PRESANT:

Q So Dr. Coble, I was asking you about general acceptance, and you were saying that you think the number of labs who are using it are evidence of general acceptance?

A I do.

Q And is your personal opinion, your personal expert opinion that it is accepted within the scientific community?

A Yes. It is.

Q And you are satisfied with the work that was done here in this case such as you can tell the Court that STRmix itself, the version at issue in this case, and its application to the case work in this case, are reliable?

A Yes.

MR. PRESANT: Nothing further. Thank you, Your Honor.

THE COURT: Dr. Coble, I just have one additional question and then I'll turn you over to Defense Counsel. You have worked, if I recall correctly, with Dr. Buckleton, who is the primary developer of this software, right?

THE WITNESS: I have -- well, when you say work, I have collaborated. I still collaborate with Dr. Buckleton in projects and so forth. For a brief period of time when I was at the National Institutes of Standards and Technology at NIST, Dr. Buckleton was there as a visiting scientist for I think maybe a year, year and-a-half, maybe two years. I can't remember exactly. However, he was in a different division than me so we really didn't interact that much when we were there.

THE COURT: I just have a question. He -- and I don't know whether it was in the earlier iteration of this hearing or someplace else, but he has been quoted as saying that he has never heard of an error that has been detected in the STRmix software. But as I understand it, that's a little bit of puffery. There have been some errors which have been detected, isn't that right?

THE WITNESS: I think there was an exhibit from the government's exhibit in the previous hearing of miscodes that were covered in STRmix, but I think maybe -- I don't know exactly what Dr. Buckleton was talking about. Maybe he was saying that the effect of that code was not a case where someone who had a high likelihood ratio went to exclusion, that kind of a thing. That, again, is where -- that's what I consider to be an error. If you have something that is here that's way, way above your likelihood ratio of one and then you find a mistake in the code or whatever, and you discover that through your actually running the software, then you fix that and it now gives you a likelihood ratio that's exclusion that would be an error, and I don't think that's ever happened.

THE COURT: Okay. He is pretty proud of the software as you might expect and as you probably know. Thank you, Dr. Coble.

We'll take a ten-minute break here and we'll come back at -- 15 minutes. We'll come back at 10 after 11:00.

THE CLERK: All rise. Court is in recess.

(Off the record, 10:57 a.m.)

(Resume Proceeding, 11:14 a.m.)

THE CLERK: Court is back in session. Please be seated.

THE COURT: Ms. Kloet?

MS. KLOET: Thank you, Your Honor.

CROSS EXAMINATION

BY MR. KLOET:

Q Good morning, Dr. Coble.

A Good morning.

Q My questions to you today are going to be tracking your report so hopefully I can stay as close to that as I can. So it will be primarily what I am asking you to reference as we are going through.

Starting with testing. In the testing section you talk about validation, both developmental validation and internal laboratory validation. Now, that validation is completed under certain guidelines that have been recommended by the FBI, correct?

A By SWGDAM, yes.

Q And you are a member of SWGDAM, is that right?

A I am an invited guest.

Q Okay. And you were a part of the group that developed those guidelines?

A Yes. I was on the -- I think I was the cochair of the task group -- or it wasn't an official committee, but of the working group that developed those guidelines.

Q Thank you. Those guidelines were published for public consumption by the community in June of 2015, right?

A I think that's right. Yes.

Q Okay. And those are informal in the sense that they are guidelines as distinguished from, I believe your testimony earlier was standards, right?

A That's right. They are guidelines.

Q Thank you. You are also a member of the International Society For Forensic Genetics, right?

A Yes.

Q And that group published recommendations for validation of probabilistic genotyping systems, right?

A That's right.

Q And you were a member or an author of the article that contained those recommendations?

A Yes. I was the chair of the DNA commission on that, that group that we published the paper on the recommendations for validation of software, not necessarily probabilistic software, but any software that produces a statistic, whether it's Y chromosome database, a Monte Carlo DNA database, anything that produces a likelihood ratio or statistic from software. These were recommendations that we developed.

Q Okay. Those recommendations were published in approximately August of 2016?
A That sounds right.
Q And they were published in Forensic Science International Genetics, a journal with that title, right?
A Yes.
Q And you are on the editorial board of that journal, right?
A Yes.
Q Does STRmix comply with all of those recommendations contained in the article you authored?
A Yes.
Q Would it surprise you if I told you that Dr. Buckleton testified just last month in Illinois that it does not comply with all of them?
A I wouldn't know which specific recommendation would not be in compliance with STRmix.
Q Have you discussed that with Dr. Buckleton?
A No. This is the first I've heard of it.
Q Have you discussed the recommendations as they apply to STRmix with Dr. Buckleton?
A Well, he was part of that group. He was part of the -- he is an author on the publication.
Q Okay. Are you familiar with the United Kingdom's forensic science regulatory guidelines?
A Yes. I am familiar with those.

Q And in your opinion, does STRmix comply with all of those?
A I don't specifically know. I mean, that's -- I was part of that -- I was asked at the time to assist the forensic science regulator, the group that basically won the contract to do this work. They first wanted to do a mixture study with laboratories that provide work in the UK. At the time the forensic science service, which was the main provider of forensic science, forensic DNA work in the UK, had been privatized and then had closed down. And so now all of the DNA testing that's performed in the UK is from private labs. And so the regulator wanted to first do a little mixture study to see how well labs are doing compared to one another so they reached out to me. At the time I was at NIST. And I had mentioned about doing this study where I sent out DNA -- the data -- the raw -- not the raw, the electropherograms to labs in the U.S. So we did a similar study in the UK except we gave them tubes of DNA. So they had to amplify and then run it on their instrument and then analyze the results. So I am familiar with their document but I wasn't part of, like, writing those standards. So I am not a hundred percent familiar with all of them, but generally familiar.
Q And so just to recap, you are not -- your answer is you are not sure?
A I am not sure.
Q Okay. Same question, would it surprise you if I told you

Dr. Buckleton testified just last month that it does not comply with all those regulations?

A I would assume he knows, so I would I guess not be surprised if he said so.

Q Thank you. I wanted to touch very briefly on your professional relationship with Dr. Buckleton over time. You testified earlier that he was at NIST for a short period of time while you were also there but in a different division?

A That's right.

Q You were an employee or paid by NIST, right, as a federal employee?

A Yes. A federal employee.

Q Dr. Buckleton was not paid by the Federal Government to be there?

A No. He was a visiting scientist.

Q Okay. He was there approximately what time frame, do you recall?

A I think it was -- I can't remember the exact time frame but I think he came in September of -- I would have to -- have to do a little thinking here. So I would say it was probably around 2016 and probably was there until maybe it was 2015. He was there for about a year, year and-a-half and maybe two years. I don't remember exactly to be honest.

Q At some point in time you were invited to attend a STRmix training in New Zealand, right?

A Yes.
Q Approximately what time was that?
A That was in 2013. That was in March of 2013.
Q Was that before Dr. Buckleton took his unpaid position at NIST?
A Oh, yes.
Q Okay. And you were there in New Zealand at a training at Dr. Buckleton's invitation, right?
A I was there for the training by invitation of ESR, which is the company that Dr. Buckleton works for.
Q Thank you. When you attended that STRmix training, they footed the bills for your expenses like hotel and flight, is that right?
A So -- yes. So they were willing to pay for the entire trip because it would otherwise be costly. So we had to work it out with NIST and ESR. And this was all done above me, my pay grade. Basically, the Federal Government would not allow me as a federal employee to take money from obviously a foreign company, but it's called assistance in kind. So they paid for the flight and the hotel, and NIST paid for all of the other, you know, meals and taxies and all the other things while I was in New Zealand.
Q Just to remind me, that was in approximately 2013?
A That was in March of 2013 I think. Pretty sure. It was right before Easter.

Q Thank you. Your CV indicates that you coauthored several articles with Dr. Buckleton and the other creators of STRmix, Drs. Bright and Taylor, right?
A Yes.
Q My review of your CV indicates the earliest article with Dr. Buckleton was in 2014. Does that sound about right to you?
A That is probably the case.
Q And the most recent was just this year in 2019?
A Yes.
Q The other articles you coauthored with STRmix's other developers followed the same approximately timeline from 2014 to 2019?
A Probably so. Yes.
Q Okay. And sometimes at least upon request you assist in providing training on this type of software to individual labs who are bringing on STRmix for example, is that true?
A So I -- excuse me. I have been asked to provide training for laboratories that are interested in bringing on probabilistic genotyping. So I will do typically one day on the likelihood ratio and then either a half or full day on probabilistic genotyping. And it's not just on STRmix. I mean, certainly we discuss STRmix, but we also talk about those semi-continuous programs. So we go through all aspects of probabilistic genotyping.
Q And is that something you are compensated for?

A So not directly. So typically what happens is the payment for the training would go to the University of North Texas and into an account. So I don't directly get compensated or paid for that training. It goes into an account at UNT, and that account would be used for, say, travel to a conference or you know, buying a printer or something like that that would then be used. So it's not a direct compensation per se.

Q Thank you. I'd like to talk about the internal validation completed in this case. Now, my understanding is that the internal validation by the MSP of STRmix was provided to you in your preparation of the report here, right?

A The validation summary, yes.

Q Right. Okay. That validation by MSP was completed in February of 2016, right?

A Okay. I'll take your word. I don't know. I don't have the document in front of me, but. . .

Q If you --

A That sounds about right.

Q Can you pull --

A I think from the audit document that was the date when the -- when the auditor said they had reviewed the protocol?

Q We'll go with that then. It doesn't sound like where you and I have a dispute.

November 2016, that was after the SWGDAM guidelines were published in 2015 but before the recommendations that you

made in your article that the International Society of Forensic Genetics were made.

A Okay.

Q Okay. You made those later on that year, right?

A Yes.

Q Okay. And the validation by MSU was also completed before the PCAST report was issued in December of 2016?

A Yes.

Q And its followup addendum was issued in January?

A In January. That's right.

Q Okay. The version that was validated by Michigan State Police was version 2.3.07, correct?

A Yes. That's correct.

Q That version was released in about 2015?

A That sounds about right.

Q But there have been subsequent versions of STRmix released, through commercial consumption anyway, since that version, right?

A Yes.

Q In the 2.3 series alone we have .08, .09 and .10?

A Okay.

Q We also have a 2.4 series and a 2.5 series. In fact, we are currently on series 2.6. Does that sound right to you?

A That sounds right.

Q All right. So it sounds right to you to think there have

probably been about 14 commercial versions of STRmix issued since 2.3.07?

A I have no idea on the specific number, but there have been several.

MS. KLOET: May I approach the witness, Your Honor?

THE COURT: Yes.

BY MR. KLOET:

Q I am handing you what's been marked as Defense Exhibit SS. If you take a look at it, can you describe what is on that document?

A Excuse me. So this is a summary of the commercial versions all of which have had a full developmental validation.

Q Does that look like a fair and accurate representation based on your familiarity with the program generally about what versions have been released for commercial consumption?

A Yes.

Q Thank you.

MS. KLOET: Your Honor, I'd move to admit Exhibit SS?

THE COURT: Mr. Presant?

MR. PRESANT: Your Honor, the witness previously testified that he wasn't aware of all of the commercial versions that are available. I don't know where this document came from, and I think Ms. Kloet just led him into saying it was a fair and accurate representation without actually laying a foundation for where it is. It may be correct. It may not

be, but as long as we are going to apply the rules of evidence here with respect to hearsay, I am going to object to this document, as well.

THE COURT: Do you have further foundational basis for the document, Ms. Kloet?

MS. KLOET: Your Honor, this document was -- I don't know if you want me to ask the witness questions, but it was obtained from ESR's website, which are connected through John Buckleton's website, which is a reference that he used in a footnote of his report. That's the foundation that I have without bringing the representative of ESR to say they published this for Dr. Buckleton.

THE COURT: I will allow it.

MS. KLOET: Thank you.

BY MR. KLOET:

Q Now, ostensibly each one of the versions before it's released for commercial consumption it must be developmentally validated, correct?

A Yes.

Q So there have been changes purportedly to each version to either fix problems or perceived problems or improve the functioning of the software, fair to say?

A I don't necessarily know if that's the case. I wouldn't say that's always true. I think that maybe there is a version that's working perfectly fine but the next version maybe

includes additional, you know, things that are easy for the user. Like, for example, one version of STRmix that I used previously you had to -- when you want to bring in the evidence or you want to bring in a reference you had to open up that folder and click it and put, you know, enter and all that. Now there is a functionality of dragging and dropping, so I can just open the folder and drag and drop those files. That may be the reason for a new version. It doesn't mean there was something wrong or errors in the previous version. It's just an improvement in functionality. So I can't say that each one of these represents a mistake or an error that was found in STRmix.

Q That's fair enough. But each version that is released is in some aspects a new and improved version that generates more sales for ESR?

A I suppose. I don't know. I mean, that's not really my -- I don't really have any insights on the sales force of ESR or anything that they are doing.

Q The version that was used here by MSP, 2.307, about a dozen back going from that list, that version did not account for a phenomenon called forward stutter in its analysis, correct?

A That's right.

Q But subsequent versions did, right?

A Yes.

Q And there are still some changes underway with the program. Do you know if the -- if STRmix creators are trying to write the program in two different computer codes to try and compare and contrast results?

A I am not that familiar with what they are doing to be honest to answer.

Q The purpose kind of broad view of an internal validation is to establish the outer limits of reliability of a particular software program, in this instance for a particular lab. Is that a fair characterization of the purpose of internal validation in your view?

A I would say it's probably in my opinion an internal validation is to determine if the software is fit for purpose. Does it work the way its supposed to work? And you challenge that system with samples that you developed in your laboratory on your instrument with your kit, and then you sort of find that -- those areas of where the boundaries are, if you will, for using the software.

Q And you find those boundaries by figuring out when it works as you expected and when it doesn't, when that starts to break down?

A Well, I guess, yeah. The language here, I am not sure I would agree, when it works and when it doesn't work. I would say if the results are providing you likelihood ratios greater than one for true contributors and likelihood ratios less than

one for non-contributors, then that's what you expect.
Q Okay. You reference on page 4 the NIST 2013 study -- and this is of your report?
A Yes.
Q Now, that study, NIST 13 or NIST 2013 revealed that 74 of a 108 labs wrongfully interpreted a four-person mixture, correct?
A I'm sorry. I was -- could you repeat your question? I'm sorry.
Q Sure. The initial preliminary results of the NIST 2013 study, that study showed that 74 out of 108 labs wrongfully interpreted a four-person mixture, right?
A So there is a difference between interpretation and the statistical weight that was provided. So I would say that the labs that -- yes. The labs that were using CPI had given a -- provided a statistic for that contributor that was actually not in the sample.
Q So in laymen's terms they provided a statistic that tended to suggest the individual was in the mixture when in fact he was not?
A Yes.
Q There was a technical leader meeting of individual labs shortly after the results of that before they were published but when they were I guess released to the community in about fall of 2013, right?
A That's right.

Q Would you say that many technical leaders were surprised by those results?

A I think so. I think that that it was -- it was a shock, I think, to the audience to see those results.

Q Do you think that -- I think you testified previously that some folks were not so surprised. Not everyone collectively shared that shock?

A Yeah. I think that's right. I think that there were some people who were -- in fact, I know, based upon the data that was provided to me from the laboratories, one laboratory commented to me that, wow, we were really shocked when we actually used these mixtures within the lab. So they did an intralaboratory study where they gave those mixtures to the 15 or 20 analysts that were within the lab and they saw a wide range of results within the same laboratory. And so it caused them to take a step back and do some retraining and rethinking about mixtures. So I think for some people it was not a surprise.

Q The results of the NIST 13 study were eventually published in Forensic Science International Genetics?

A That's right.

Q However, they weren't published until 2018. Why the five-year delay?

A So I of course having conducted this study and then seeing the wide range of results, what had happened, this was a

two-day meeting. This technical leader summit, if you will, was a two-day meeting. And the first day we presented the results of the study. And there was a lot of people very upset. There were some people who weren't surprised. And so what the feedback I had heard from that first day was, you are telling us we are doing things wrong. What are we supposed to do? What are we supposed to do?

Well, if you remember, I said in March of 2013 I went to New Zealand and I had a copy of STRmix on my laptop. So at the end of that first day I went to my room and I ran these mixtures through STRmix. And the next day I gave a presentation about probabilistic genotyping. And I showed that if you used STRmix and other programs since then, it would have excluded that person. It would have been given a likelihood ratio of zero. He is not there. It may look like he is there but he is not there.

So at that point I felt a responsibility -- and I didn't stop talking about Mix 13. I continued to give presentations on it both to scientific conferences with forensic scientists. I spoke about this at the innocence conference. I spoke about this for the public defenders. I spoke about this to everyone. I spoke at Barry Scheck's law -- Cardozo law school. Barry Scheck puts on a summer DNA. I presented there. But what I did, what I was focusing on for several years between 2013 and the publication is familiarizing

the community with probabilistic genotyping and showing why I felt this was a better way to interpret mixtures.

Q Between 2013 and 2018, when the results of that study were published, many labs did continue to use CPI for these types of samples that were evaluated in the study, correct?

A Yes.

Q Okay.

A I'm sorry. That's probably a question that I can't just answer with a yes. But, if you don't mind just saying, labs that were not applying CPI correctly, yes. Labs that were applying CPI correctly, they were fine. So one thing that we did in Texas, because Texas we had a full review of lots of, like, 40,000 cases, where we went back and looked at cases that used CPI. And so as an output of that, myself, John Butler, John Buckleton, Fred Bieber, B-i-e-b-e-r, and Bruce Budowle, we published a paper about this is the correct way to use CPI as a way for labs to move forward that will want to continue to use that method.

Q Thank you. Now you, Dr. Buckleton and Dr. Bright, who are for the Court's reminder the developers of STRmix, then prepared a paper addressing the Mix 13 study. And that was published in the same journal, the same volume even, just a few pages later, and that's what you attached to your report in this case?

A Yes.

Q Great. Do you have exhibits to your report or no?
A I'm sorry?
Q I am not sure if you were given the exhibits to your report or if you were just given the report. If not I will pull up your exhibits. It doesn't look like it. Can you pull up?
A I think I have it. Yes.
Q You do have it. Okay. All right. So the first exhibit you attached is that followup Mix 13 study that you are the coauthor you helped Buckleton write?
A Yes.
Q All right. I want to turn your attention to page 173. The first full paragraph. If you could read the first three sentences into the record, please? It starts with discussion of.
A Okay. Discussion of Mix 13 continues. This work and previous presentations confirm that the translation of mixture interpretation theory and practice to the bench analyst was ineffective as of 2013, and resulted in some laboratories inappropriately interpreting mixture data. These findings are not contested by the forensic genetics community but neither do they shed light on the current state of mixture interpretation as of 2018.
Q Thank you. Is it true that since the study was conducted in 2013, the interpretation matters, models, methods have changed substantially? For instance, there are newer

multiplexes available?
A Yes. That's true. And I would also add that at the time in 2013, there were only two probabilistic software systems that were actually used in that study. So out of the 108 labs there were only two that used a probabilistic and actually one lab didn't use it for every sample, just one of the five samples. So yes, I would agree with you on that.
Q Thank you. There are other software that's at play in the analysis of DNA material in a particular lab, true?
A I'm sorry. There are other software?
Q Yeah.
A Yes.
Q There is the amplification software. Like PowerPlex Fusion would be one brand for example.
A Well, Fusion is a kit. It's not really a software.
Q Can you explain the difference?
A So the kit contains all of the reagents and materials that are used in the preliminary chain reaction of the PSR reaction. So basically you extract the DNA from the sample and then you add some of that DNA into this tube that has that material from that kit, and that will amplify and produce the profile, those peaks that you see on the electropherogram. So the kit itself is not a software but there is a software that's used to basically translate that information from, think of it as an analog signal into a digital signal. So you have these -- this

tube that has this DNA that's been amplified. You can't really see is that a 6/9.3. It's not until you separate it on that capillary instrument and use that software that will tell you this is a six peak, this is a 9.3 peak, and so forth. So the kit itself isn't a software but there is software that's used to analyze that result.

Q And the software used to analyze the result, would an example or brand example of that be GeneMapper ID-X?

A Yes.

Q Okay. GeneMapper ID-X is up to version 1.6 now, correct?

A I think that's right, yeah.

Q And the kits also go through upgrades as time wears on?

A That's true. We have expanded the minimum number of loci that need to be tested in the U.S. from 13 to 20. So that's an update.

Q Thank you. And back to your Exhibit 1 to your report. This is the Mix 13 study, the second one. I'd like to call your attention to page 178. And I am looking at the conclusion section. And I'd ask you to just read that first short paragraph into the record, please?

A I'm sorry, under the conclusions?

Q Yup. Where it begins Mix 13.

A NIST Mix 13 is of historic interest. However, interpretation methods have been strengthened or changed substantially and there are newer multiplexes since 2013.

Moreover, the outcomes of cases three and five should be considered within this context on how they were constructed and because of this the outcomes do not provide an accurate assessment of an analyst's performance but do provide an interesting example of the limitations of DNA profile interpretation.

Q Thank you. I'd like to move onto the peer review section of your report, beginning on page 2. In that section you cite to an article that summarizes the results of some internal validations of STRmix. And I think the language you use is this constitutes, quote, an excellent example of independent peer review. Is that an accurate reflection of what you stated?

A Yes.

Q Thank you. This independent peer review summary was completed in 2017, right?

A I'm sorry. Could you repeat?

Q Yeah. The summary itself was completed in 2017 and then released for publication in 2018. Does that sound about right?

A I am not sure what you mean by summary. The summary of?

Q I'll say the article. The article itself was written in 2017 and published in approximately 2018?

A Okay. So we are going back to the Exhibit 1, is that true?

Q It would be the internal validation of STRmix that the government previously offered as government Exhibit 4.

A Okay. Yes. That sounds correct.
Q Okay. In this -- in your testimony responding to the government's questions, you described a graph showing where they ran a three-person mixture that they knew to be a three-person mixture as a four-person mixture.
A Right.
Q Can you show me in this study where it shows they ran a four-person mixture that they knew to be a four-person mixture as a three-person mixture and what effect that had on the likelihood ratio?
A I would have to -- I would have to look at the paper. I don't -- I don't recall off the top of my head.
Q If you want to take a look at your screen, I believe we pulled it up, the government's previously admitted Exhibit 4. And I think if you -- can we make it bigger, the whole page?
A So this is the government Exhibit 4.
Q And this was part of the materials you read in preparing your report?
A Yes. I am sorry. So your question was is there examples of underestimation? So it's a four but they ran it as a three?
Q Correct.
A So the -- in figures four, five and six they do show examples where running as different number of contributors the effect on the likelihood ratio. So these are violin plots.
Q Can you explain what those violin plots mean in terms of

results?

A What a violin plot will show you is a way to visually look at data. So let's say for example I ran -- I ran STRmix with a non-contributor a million times. And I got a lot of -- a lot of data points. So a million points of data. Now, if I just show this as here is -- so I'll do this. So here is my line. This is the likelihood ratio of one. Anything before one is here. Anything below one is here. And I have a million data points. Now, if I put a million dots on this line and all of the likelihood ratios are around one, you'll just see a blob. What the violin plot does is it sort of spreads those dots out so you can sort of see the figure that you've got up here.

This is -- it's a little bit different than what I have for exhibit -- I think this is government Exhibit 4. I can't really -- so this is figure four. Okay. So what we are showing here on the first one is the dark part of this violin plot is showing the likelihood ratios from true contributors, people who are actually in the mixture, and then in the white sort of part are non-contributors. So these are people who are not in the mixture, and you are seeing that about 30 percent of the data are represented in this violin plot.

So if you -- again, it's hard for me to find, but it says in this paper, the figures four, five and six with additional information regarding the consequence of over or underestimating the number of contributors, the power -- the

under -- I am skipping down. Also consistent with previous findings, and it says 18 as the reference. The underestimation of the number of contributors either tends to either have little effect on the likelihood ratio or will tend to exclude known contributors.

Q Just to be clear, you are on page 18 of the 35 page document?

A I think that's right. Yes.

Q Okay. Can you turn to page 25 of that same article, please, in the government's exhibit? Might be easiest to follow along that way.

A You said 25, I'm sorry. Yes.

Q PDF 25?

A Okay.

Q And in the third paragraph up, the third full paragraph up starting with the word underestimating, can you read that first sentence into the record for me, please?

A Yes, ma'am.

Q Thank you.

A Underestimating the number of contributors can result in false exclusions of true donors. In this study this is seen when apparent N is fewer than true N.

Q I think that's fine. Thank you. My focus was on the first sentence. So if there is an error in the determination of the number of contributors, this means that someone who is actually

in the mixture could be wrongfully excluded from that mixture, correct?

A There is an -- it's -- from what I have studied myself, there is a slight risk that underestimating the true number of contributors could lead to a false exclusion.

Q Okay. Thank you. And that's essentially what the article says without the qualifier?

A True.

Q Thank you. Now, this article that we were just looking at, government's Exhibit 4, that was also published in Forensic Science International Genetics, correct?

A That's right.

Q And the coauthors of that article included Drs. Bright, Taylor and Buckleton?

A Yes.

Q Thank you. And there is one more reference I wanted to make in that article. I apologize.

A I am not part of that study, just to note.

Q That's correct. You are not. Let's see. Give me one second here. Actually, I am going to move on.

Now, that study summarized the results of 31 individual labs validation of the STRmix program?

A Yes.

Q All right. That study took the data that they produced but it did not double-check the parameters that were established

prior to the running of STRmix by the labs, correct?
A Well, they took the likelihood ratios I assume. I can't remember exactly all of the things that they did, but yes, I think they took the outputs from those. They knew the ratios. They knew the amount of DNA. They had all of that information and the likelihood ratio result.
Q So it didn't double-check the lab's conclusion as to what, for instance, the drop-in rate would be or the drop-out rate or other sort of lab specific parameters that are input into STRmix?
A So there is no specific drop-in, or I'm sorry, no specific drop-out rate that's put into the software. That's something that the software models. So there is not a physical number that the lab would enter. Very similar for drop-in. It's modeled so these are not parameters that you physically enter into the software where you are setting up the example to say, okay, use a drop-out rate of this or drop-in rate of this. These are things that the software will model.
Q And those numbers are determined through the individual labs validation?
A So those parameters get determined through the validation study process of STRmix.
Q Okay. And that's not -- that wasn't the purpose of this 31 lab summary, was it, to go back and make sure they calculated those correctly?

A No. Not to my knowledge.
Q Okay.
A But I wasn't part of it so I don't know specifically.
Q All right. Thank you. You talk in the first paragraph of your report about how two different -- I believe it was the first paragraph. Maybe not. It's somewhere in your report. I'll find it in a second. You talk about two competitors actually use the same modeling as STRmix?
A I think that there is actually more than two at the moment. There are different ways when it comes to this continuous method of interpretation, continuous models. There is some software that uses what we call a Markov Chain Monte Carlo process. And what they are doing is basically a lot of simulations to try to come to what makes the most sense to explain this mixture.

There are other software programs that actually try what I call a brute force way. They actually look at the peaks that are there and model what would happen if the drop-out was this. What if it was that? What if -- so it's doing a brute force modeling of one RFU at a time coming to try to come to that same convergence. And you saw from that publication by the Italian group, even though they are different models being used, they are all sort of arriving at the same sort of conclusion. So yes, there are several competitors or several software systems that will use this Markov Chain Monte Carlo,

not just STRmix.

Q So if you could turn to page 2 of your report just under the peer review section in the first full paragraph of that section and read the last sentence that starts with, in fact?

A Oh, yes. In fact, two competitors of STRmix, GeneProof and MaSTR, use the same mathematical modeling and approach of STRmix.

Q Okay. And is it your testimony today that there is more than two?

A Yes. So I didn't mention, but also the other competitor is TrueAllele. And then there is another one that I think this is actually in my review paper that we published last year that has a list of all the available software programs. But there is another program called DNA Mixtures that uses a Markov Chain Monte Carlo. So that's at least five that I am aware of at the moment that do this MCMC process.

Q TrueAllele uses the MCMC process, but they are, for lack of a better word, calculation processes. Not exactly the same as STRmix is, correct?

A Different models -- different programs have different models.

Q Okay. So TrueAllele does have some different modeling than STRmix?

A Yes. That's why you can get different results from -- and that figure -- again, I'll come back to that Italian group.

You can see they are not exactly on top of one another. There is a little bit of spread. So there is some difference, and that difference is due to the different models that are being used.

Q Approximately how many PGS programs are out there? I think if you take a look at -- I think you attempted to address that question in Exhibit 3 to your report. Is that fair to say?

A Yeah. I mean, today is Monday. I think there is probably at least 13 or 14. There may be one more tomorrow. I mean, there are constantly programs coming out. Some of them, again, are continuous models like STRmix. Some are semi-continuous. But it seems to me that the semi-continuous models are -- not that there is anything wrong with them, but they are just not as efficient because they don't use the peak high information and they don't model things like stutter. So an analyst has to decide is this a stutter peak and if it is they'll click it off. If it's not they'll keep it in.

THE COURT: Let me just ask, if I understood your testimony a little while ago that the competitors that use the continuous method, even though they may use different modeling to reach their results, it's your view, based on the study, that they come out with very similar results?

THE WITNESS: Yes, ma'am. That's -- that's -- that's what I have observed in my own studies that I have done with probabilistic software in the past. When I was at NIST I had

the ability to look at, interrogate these different software programs, and that's generally what I would see is when I would run a sample with STRmix and I would run it with TrueAllele you typically get the same answer maybe within one or two orders of magnitude.

THE COURT: And -- can you give me a time parameter when probabilistic genotyping became a mature form of DNA analysis?

THE WITNESS: Well, I think I would look at the history of publications of STR testing and typing, and I would say that in the year 2000 there was the first publication that gave a probabilistic approach to interpretation. And that was created -- that was then made into a software program in around 2006 or so. It was a software program by the Forensic Science Service, and it was called Locomation. And so that was sort of the first sort of software that came out was around 2006. And then there are others that came out in 2007, 2008. The continuous methods, TrueAllele really started being publications about the methods of TrueAllele in 2009, 2010. So we are talking about a decade ago when these were first started sort of coming out with actual software available. And then just in the last three or four years there's been an explosion of different software.

THE COURT: And the historical purpose behind the development of this software is specifically to be able to

analyze mixtures of DNA that exceed two. Is that fair or not?

THE WITNESS: Well, I would say today, yes, that's pretty fair to say. But I think the real genesis of this method, this probabilistic approach has to do with the stochastic threshold. There was a recognition by the European community, the ISFG, which is based in Europe, they published a paper in 2006 that said you need a stochastic threshold, because you need to be aware when you may have missing data. But they also note in that paper that stochastic thresholds have a problem in that here is my stochastic threshold. Here is my peak. Let's say this line is 300 RFU. Here is my peak at 301. I can call this peak with some confidence that it's a homozygous, in other words it's a 6/6. 301. 299. I can't call it homozygous anymore. I have to call it 6 something else. Maybe drop-out. So they recognized in 2006 that there has to be a better way.

In 2010 the U.S., by SWGDAM, said labs should start using a stochastic threshold for mixtures.

At about this same time in 2006, 2007, 2008, there was a shift in the kinds of cases that were being submitted to laboratories. So predominantly mixtures back in 2006, 2007 where two-person mixtures. Mostly high quality, high quantity blood, you know, blood on a sidewalk or a sexual assault where you get lots of sperm. Maybe a little bit of female. So those are most of the mixtures. But starting around 2004, five, six,

there was a recognition that we can get DNA from materials that, quote-unquote, have been touched, like steering wheels and you know, cell phones and guns and things like that. So it was a shift in the types of cases that are being submitted. And what happened in that shift is that we started seeing more and more complex mixtures. More than two, three, four and more.

So yes, when you get to three and four-person mixtures, my recommendation when I do training is if you got a three-person mixture and you don't have software, I only feel safe interpreting that if there is a real high major and some real low minors and I really don't care about the minors but I am real interested in the major, that's okay. But if you are going to do anything more than that, you really need software. And so that's sort of where this probabilistic software has helped in that respect.

THE COURT: Thank you.

MS. KLOET: Thank you, Your Honor.

BY MR. KLOET:

Q I'd like to turn to section three of your report addressing error rate. So for STRmix to operate in the version that was used in this case, you have to, you being the analyst have to determine or assume or estimate a number of contributors, correct?

A Yes.

Q And this is, in fact, can be a critical determination by an individual analyst?
A Yes.
Q STRmix version 2.6 allows for the introduction of several potential numbers of contributors, correct?
A It will allow some flexibility, one up or one down in number of contributors, estimated.
Q So that would produce ostensibly a likelihood ratio for each possible?
A Yes. Yes.
Q Okay. You testified earlier about your own experiences comparing non-contributors to mixtures. And I guess we call that interrogating the mixture with non-contributors?
A Yes.
Q Okay. The theory being if you get a high likelihood ratio back for a non-contributor, you are looking at the possible false inclusion of that profile because you know that person is not in there, right?
A If you get a high likelihood ratio for a non-contributor? Is that what you started with? Yes.
Q Right. Okay. So in terms of trying to get a reliable answer out of the program like STRmix, let's consider the converse situation. Let's say you have a non-contributor or a non-contributor or two in the mixture. Would inputting the profile of a known contributor or contributors be useful

information for the STRmix analysis?

A It's possible. It depends. Like for example in a sexual assault case you may have the vaginal swab from the victim and so it can be assumed that she would be on that swab. So you could condition, if you will, condition that the victim's profile is in the mixture. That may help if the victim is really really high. It may make no difference if she is the real high major and the minor is the person of interest. Then assuming the victim may make no difference whether you do or you don't, because the software is able to easily identify this major contributor.

Q Okay. That's something you discuss in the Exhibit 1 or attachment one to your report in that article, the Mix 13 part two. And I am calling your attention to page 175. The first column, the paragraph that begins with, some practitioners. And I'd ask you to read that second sentence based on case circumstances into the record, please.

A Okay. Some practitioners in the U.S. and in the NIST study generally have not considered to condition on a consensual partner or even at times on a victim even with reasonable expectations of either or both of them being a contributor such as from an intimate sample for mixture interpretation. Based on case circumstances, it may be reasonable to assume certain individuals as known contributors to a mixture.

Q Thank you. You can stop there. So in essence what you are

trying to say is it depends on the particular case at hand, but having this information might help with the analysis of, for instance, the number of contributors in the mixture, fair?

A I am not quite sure I understand your question, so --

Q Sure. I'll rephrase. So if you have an electropherogram that you are trying to determine or estimate the number of contributors in that mixture, and you know with certainty or as best certainty as you can get in a real case example, that there are at least -- at least two, you know, contributors to that mixture, and that's undisputed, you know that the number of contributors is going to be two or more most likely, is that fair?

A Well, I don't know of many labs, if any, that would make that kind of an analysis up front. I think that there may be knowledge that this is an extraction of the victim's underwear. So maybe there is -- you know, you at least expect to see one person. But it's not until you actually look at the data that you sort of do that sort of independently determine the number of contributors.

Now, when it comes time to setting up your propositions for your likelihood ratio that you are going to be using STRmix for, knowing information, case information like for example, this is a sexual assault. We see what looks like to be at least three individuals in this mixture, and we know that the victim has said that she and her husband had sex the

day before. So it may be reasonable to assume her and her husband and then one other unknown if the determination is this is at least a three-person mixture.

Q Okay. Thank you. On page 3 of your report you address the error that was discovered -- and actually I think it was section 3, page 4. Sorry about that. The error that was discovered in the Mix 13 study in a program called EuroForMix?

A Yes.

Q You stated in your report that this error was not found by a code search, is that right?

A That's right.

Q The code search or review was not the purpose of the Mix 13 study back in 2013, right?

A No. It wasn't.

Q And you as a forensic scientist are not engaged in the business of code review. That's not something you are doing on a day to day --

A No.

Q You also stated in your report that EuroForMix is open source and freely available, is that right?

A Yes.

Q And STRmix is not open source and in the same respect that EuroForMix is, right?

A Yes.

Q Okay. I have a hard copy of this if it'll make it easier,

but I have pulled up on the screen here proposed Defense Exhibit TT?

A Okay.

Q This is -- can you identify this? Have you seen this before?

A Yes. We talked about this paper earlier. This is the paper from the Italian group. Alladios, A-l-l-a-d-i-o-s. First author.

Q Okay. And I have a hard copy if you need one, but you are able to see it on the screen. This is the same government Exhibit 37. I can bring you a hard copy if you'd like.

So I want to ask you a couple questions about this Alladios study. This was a study of both semi and fully continuous probabilistic genotyping --

A That's right.

Q -- systems, right? And STRmix is a fully continuous model?

A Yes.

Q So I'd like you to turn to page 145. And if you could take a look at section 3, results and discussion? The second full paragraph of that if you count one, two, three sentences down the sentence begins with, LR results. LR results provided. Do you see where I'm at?

A Not quite. Oh, yes. I see now. Yes.

Q Okay. Could you read starting from, LR results provided, that part to the end of that paragraph only, please?

A Okay. Excuse me. LR results provided by both semi-continuous models were very similar or identical. This is due to the fact that LabRetriever and LR Mix Studios software utilizes similar algorithms with a slightly divergent formula. Furthermore, log LR results provided by fully continuous models proved similar and convergent to one another with slightly higher within software differences, i.e., approximately three to four degrees of magnitude.

Q So I'd like to focus on that last parenthetical, approximately three to four degrees of magnitude. Let's put it into dollars. I think that'll make it easier for me to understand anyway the difference between -- so the difference of four degrees magnitude. And if we start with, say, $400, one degree of magnitude would be $4,000, right?

A Okay.

Q Two would be $40,000, three would be $400,000, and four degrees of magnitude would be four million dollars?

A Okay.

Q So this sentence indicates that there is -- that's a pretty I guess would you agree relatively speaking but for your average middle class citizen a pretty -- pretty distinct difference between the value of $400 and four million dollars, fair to say?

A I do this example when I teach probability and I ask the question how much is a lot of money? And people will say a

million dollars. And I say, when my kid comes up to me wanting $20 I say that's a lot of money. So I guess it's all in the eye of the beholder.

Q It's relative?

A Yeah.

Q But this sentence indicates within the same software you are looking at differences for some of about four degrees magnitude, right?

A That's what they found.

Q For fully continuous software?

A For the different models that are being used. And I will note that STRmix is a fully continuous program that uses the Markov Chain Monte Carlo. But the other two software programs used in this study do not use the Markov Chain Monte Carlo. So it may be a little bit of an apples and oranges. Yes, they are fully continuous but they have different approaches. And sure, I mean, I will be the least shocked person to hear that I got one result with one software and a different result with another. I expect that. They are not the same software with a different label on the box. They are all different.

Q Okay. Thank you. I'd like to call your attention to page 149 of that same report. So looking in the conclusion section, if we start with the paragraph that begins with thanks.

A Yes.

Q Okay. That's pretty dense language here. And we go to, I

think it's the third or it's the fourth full sentence that starts with log LR?

A Yes.

Q Can you read that sentence and the next one, a plausible explanation, into the record, please?

A Okay. Log LR results provided by the tested fully continuous software, i.e., DNA-VIEW, EuroForMix and STRmix, turned all ways significantly higher than the ones calculated by the employed semi-continuous software, i.e., LabRetriever, and LR Mix Studio.

Q And then the next sentence?

A A plausible explanation of this might be related to the different semi and fully continuous algorithms.

Q Thank you. Right above that paragraph under table 2, if you look about halfway up that paragraph there is a sentence that begins with the phrase, in particular.

A Yes.

Q I'd like you to read those two sentences in particular and the one right after that.

A Okay. In particular, semi-continuous approaches delivered a moderately strong support to HP while fully continuous models delivered an extremely strong support to such hypotheses. In the present case the result reported at the end of our interpretation process supported the prosecution hypothesis charging the POI as an effective contributor to the biological

evidence collected on the visor of the cap that was recovered on the crime scene.

Q And if you would oblige, the next two sentences, as well?

A Okay. In our opinion, results reported in table 2 represent once again a proof to the concept that fully continuous models might be more sensitive than semi-continuous ones in case of LT DNA, that's low template DNA, mixtures interpretation. In the present case work fully continuous log LR values always supported the prosecution hypothesis.

Q Always supported the prosecution hypothesis. That would be fully continuous software they are talking about there?

A For the example that they made for this particular study.

Q And I promise I'll have you stop quoting soon, but if you can turn to the next column of the same page long paragraph there is a sentence just past the middle that starts, starts with the word, despite this fact.

A Did you say it's about midway or so?

Q Yeah. It's about midway, a little bit past midway. If you see the footnote 50 in the text just go past there.

A Yes. Okay. Starting with despite. Yes.

Q So if you could read the next two sentences, please?

A Okay. Despite this fact, extreme caution has to be used when interpreting LT DNA mixture, especially when different algorithms and probabilistic approaches are used and compared by forensic experts. Consequently, in our opinion, a

conservative approach might be employed at the current stage in order to avoid false conclusions that could eventually lead to unwanted severe legal consequences.

Q And finally the next two sentences and you are off the hook.

A For this reason, due to the complexity and the relevance of the task, a statistic redundancy in the calculations might be useful, i.e., like our adopted statistic consensus approach. Further studies will be performed in order to combine the likelihood ratio results provided by different software and algorithms using different interpretation weights.

Q Thank you.

MS. KLOET: Your Honor, I am not going to move to admit this exhibit seeing as it's already been admitted during the government but I am finished with it.

THE COURT: All right. Thank you.

BY MR. KLOET:

Q So I'd like to turn back to your report. Page 3, paragraph 3, we are still on error rate. Now, you state in your paragraph I guess it would be one, two, three, the fourth full paragraph, that it's your opinion that false conclusions are expected and they are therefore not errors, right?

A Yes.

Q And this is -- by chance this is the fortuitous match I think you term it?

A Yes.
Q So I'd like to break that down by comparing it to a different situation, if this was in the context of a test about whether or not a person had breast cancer for instance. A false inclusion would be equivalent of a false yes or false-positive diagnosis for breast cancer, right?
A Yes.
Q And that result of the test would ostensibly be used by the person as at least one factor in deciding whether or not to undergo treatment including chemo, radiation, possibly surgery?
A Potentially.
Q And all of the side effects that go with it. And your position is that potential error or that false inclusion or the false-positive is not an error and is something we should expect and tolerate?
A I would say it's only one piece of the puzzle. You know, I will just personally, my daughter came home from spending a semester at Oxford a couple weeks ago and she had a really bad sore throat. And I looked at her throat and I said, I think you got strep. Let's go and get the strep test, which was negative, but the culture they did a week later was positive.

So do these things happen? Yes. But she didn't get better after a couple of days of, oh, well, this is probably a virus so we were a little bit more aggressive in the treatment process and so forth. Went back to the doctor.

So yeah. I mean, these are -- obviously there is the potential for having false inclusions and false exclusions but what you expect with software as opposed to things like a medical test or a clinical type of test is that we have this sort of bar of likelihood ratio of one and you expect that people who are not in the mixture to give likelihood ratios less than one. You expect people that are in the mixture to give likelihood ratios greater than one. When you are at a really really low level you are going to converge. Both contributors and non-contributors will converge to likelihood ratios of one.

Q And some of the decisions relied upon or made by each respective expert, whether it's the software, whether it's the doctor in this case, I mean, they are estimates and they are subjective?

A Probabilities, yes.

Q Okay. I wanted to talk generally about auditing as part of the error rate discussion. One of the issues with the auditing of individual labs is there really haven't been very many clear-cut standards to follow, only informal guidelines such as the probabilistic genotyping, at least when it comes to probabilistic genotyping. Is that fair to say?

A Yes. There is no current standards that are recognized as being standards that a lab can be audited against in the forensic community. That's, I think, fair to say

internationally. I don't think that's just a U.S. issue.
Q So what the auditors are essentially doing is really just saying, well, do you have some sort of procedure in place that's what they are looking for as part of their auditing process?
A So yes, I think the process is they are checking to make sure that they have the ability certainly. I have been in enough audits to say that they cart in all of the binders for the validation studies and they do have the opportunity to look through those. Typically they'll look through the summary. That's the easiest sort of way to summarize what's been done and so forth.
Q Okay. You have actually been kind of critical of labs in the past for the auditing process and have advocated affirmatively for improving such standards, is that right?
A I certainly think that there is a need for more standards for when it comes to mixture interpretation than currently what we have. And those are in the process. The FBI is updating the quality assurance standards. And of course, the OSAC has also submitted several standards.

I think there is one standard at the moment for mixtures that has been produced by this American Academy of Forensic Sciences standards board, the ASB. To my knowledge there is one standard already out there that involves mixtures.
Q Do you know when that was released?

A I think it was last year, like late last year.

Q Okay. I'd like to move to section 4 of your report, general acceptance.

THE COURT: Let me just ask you, Ms. Kloet, how much longer are you intending? The only reason I ask is that I am going to take a break for lunch. If you are going to be a little while I'll break now. If you are going to be relatively brief -- because I think I've only got one or two additional questions for Dr. Coble myself. So I'd just kind of like to have a little lay of the land in terms of scheduling?

MS. KLOET: Sure, Your Honor. I've got two sections of the report left. I estimate general acceptance probably be 10 minutes or less. Application in this case maybe 20 minutes to a half an hour, so I am happy to do as the Court pleases.

THE COURT: I think maybe we should break now. It's 12:30 already. Let's come back at 1:15 and be ready to conclude with Dr. Coble and then move onto -- move onto Dr. Krane.

MS. KLOET: Thank you.

THE CLERK: All rise. Court is in recess.

(Off the record, 12:31 p.m.)

(Resume Proceeding, 1:23 p.m.)

THE CLERK: Court is back in session. Please be seated.

THE COURT: Ms. Kloet?

MS. KLOET: Thank you, Your Honor.

BY MR. KLOET:

Q Welcome back, Dr. Coble.

A Thank you.

Q I want to follow up on one of the government's earlier exhibits. It will be the government's Exhibit 37. Now, this was the manuscript that are the authors from Canada.

A Yes.

Q All right. And you indicated that you were familiar with at least one if not two of those authors, right?

A That's right.

Q Now, are any of those authors affiliated or employed with the ministry of public security with the government of Canada?

A I don't honestly know. I don't think so. The lab in Montreal is an independent laboratory for, I think, the city of Montreal.

Q Okay. So it's a municipal laboratory?

A That's my understanding.

Q All right. Would you mind turning to page -- it's marked page 1 at the bottom right corner but it's technically page 2 of that document, but there are five names and five e-mail addresses at the top of this article, correct?

A Yes.

Q And all of those e-mail addresses end with a QS.CA?

A That's right.

Q Does it appear to you that those are e-mail addresses associated with a government agency of some sort?
A It could be the, you know, province government agency I guess.
THE COURT: I think that's the country designation.
THE WITNESS: The dossier Canada.
THE COURT: Yeah.
THE WITNESS: QC is probably Quebec.
BY MR. KLOET:
Q The annotation g-o-u-v, does that have any significance to you?
A It could be government. I don't know. I am not familiar with their --
Q Do you know affirmatively one way or the other if any of these individuals are affiliated with or employed by a government agency in Canada?
A I really don't know. I don't know that much about them personally where they work. I just know them from seeing them at conferences and so forth.
Q So it's possible they work for a law enforcement agency of some sort?
A Again, I have no idea. Possible. I don't know.
Q Okay. Thank you. You don't need that exhibit anymore.
I am going to move on or start up again with your report. I am looking at section 4. In section 4 you address

general acceptance of STRmix in the relative community, right?
A Yes.
Q And your position summarized is that the relevant community that regulates STRmix is the forensic DNA community, right?
A That's right.
Q And concedingly at the end of the day that is the subject matter we are talking about here in some sense, DNA analysis?
A I'm sorry, if you can repeat?
Q That is the subject matter at issue here, DNA?
A DNA mixtures, yes.
Q Okay. And that's something that forensic analysts do is analyze DNA, right?
A Yes.
Q Yet this is a software program, correct?
A Yes.
Q And software programs contain software code?
A Okay.
Q Yes.
A Yes.
Q And the code is continuously updated and in cases like STRmix?
A I suppose. I am not a coder, so I would assume that things get updated and new features are introduced.
Q And when you introduce a new feature, ostensibly that would involve a change or modification to the change of the code of

some sort?
A Possibly. It really depends on what's being done. So I imagine yes. Again, I don't know, but I imagine adding that functionality of instead of having to go and open a folder to pull in a sample to just drop and drag I assume that would be a change in code. That would do that, but I don't know.
Q Thank you. This software, STRmix, employs millions of statistical calculations, right?
A It's -- potentially, yes. It's doing hundreds of thousands of calculations, yes.
Q And that uses a statistical model that varies from others that are available on the market or off market in the field, right?
A That's my understanding, yes.
Q And that software, which employs statistical calculations, relies upon population genetics databases to arrive at an estimate likelihood ratio figure, right?
A Yes. The population genetic database is one component of generating a likelihood ratio.
Q So do you object to including within the relevant community for general acceptance people who code and test software?
A Do I object to people in the relevant community who code software?
Q Do you object to -- I'll rephrase. Do you object to including in the relevant community for whether or not STRmix

is generally accepted people who code and write software?
A Well, again, I don't know exactly. If I were to find a computer coder and show him the Balding and Nichols' formula if they would be able to understand what that meant. It's just like me looking at computer code. I would probably end up drawing little figures and tick-tack-toes on it because I don't really read code. I don't know what it is.

So I think that what we are talking about is more of things that would happen in the developmental process, not so much in the internal validation process. I don't really see any use for someone who is a coder to be part of the internal validation. In fact, in that ISFG paper FSI Genetics, a DNA commission paper, we mention that simply just talking about computer code is not really a worthwhile exercise in court proceedings. We think that that's more of the developmental part not so much on the internal validation.
Q In validating software, which for ease of description I'll use the word testing, would a software specialist be able to test the code or run it against principles of software testing better than someone who specializes in, say, exclusively forensic DNA?
A Again, it's a little bit beyond my wheelhouse but I would say sure. Why not? I mean, they are the ones that are testing code. They probably know better than putting me in front of the computer screen.

Q You just answered your own question. How about people who specialize in statistics? You reference the Balding article. Do you think -- and how difficult would it be for your average coder to understand those principles? Do you think it's important to include statistics specialists in this community as well if it's difficult for other disciplines or persons of other disciplines to understand those principles?

A I am really not sure what -- so if we are talking about STRmix, John Buckleton is one of the foremost statisticians in the world in my opinion when it comes to forensic testing, so sure. I mean, I would say yes, there is a statistician that's part of that team. Duncan Taylor is also recognized as an expert in statistics so -- and Dr. Bright, too, so. . .

Q So to be clear, it's your opinion that Buckleton, Bright and Taylor are all statistics experts?

A I think that Dr. Bright has a Ph.D. in statistics. Dr. Taylor has recently finished a Ph.D. in statistics, so. . .

Q What about other statisticians who aren't a part of developing STRmix, would they be an important voice to be heard?

A Yes. And in fact, it's my understanding that for STRmix that Dr. Bruce Weir, from the University of Washington, is a consultant. Dr. Ian Evett, who I think is the father of likelihood ratios for forensic DNA testing, is also a consultant. So they do consult with other people outside of

ESR.

Q Knowing that those individuals are involved, I guess based on your testimony now, is it still your position that only the forensic DNA community should determine whether STRmix is generally accepted?

A Again, I think we are talking about two different things. I mean, I think if you are talking about developmental validation, that's one thing where it's nice to include statisticians, coders, whatever, you know, when you are developing a software, as opposed to the internal validation of the software, which I think is best conducted by the people who are going to be using the software. They kind of have the expertise in developing the mixtures and then, you know, understanding the problems rather than calling a local statistician from the university to come and say, you know, what should we do for our validation study, that kind of thing.

Q To be involved in developing and testing you have to have some sort of access to the STRmix program, right?

A To be involved?

Q In the developmental validation or the development itself of STRmix, you have to have some sort of authorized access to the STRmix program, right?

A To be involved in the development of the program you would need access. I think that would be fair. I mean, it's not an open source program. So yes, they have, you know, protections

in place that not just anyone can come in and mess with the code.

Q And that's what I was getting at. Thank you.

You also reference in your report that 45 labs currently using STRmix as proof of general acceptance. Now, these are mostly state labs, right?

A Local, state, federal labs in the U.S. There are also three in Canada that we usually include those.

Q These labs, they are working generally speaking at the behest of law enforcement authorities when they are asked to evaluate a sample, right?

A Well, I don't know. I think that there is some labs that would be included in this list like the Houston Forensic Science Center in Houston, which is an independent lab, independent of the police. So if they are not yet one of the labs on this list they are one of the 68 that's in the process of validating, but --

Q Generally speaking, most labs, I think this is from page 2 of your report, that most labs performing case work are generally too busy to engage --

A So I guess to answer your question, most of the labs that are using STRmix are part of government labs.

Q These labs paid for STRmix in most cases, right?

A Either they directly paid or they wrote grants to pay for the software.

Q And in on-boarding the software they were trained or had some level of involvement with STRmix staff or more specifically ESR staff?

A That's my understanding.

Q Okay. And some of them may have been trained by you on probabilistic genotyping or STRmix at the lab's request, right?

A Maybe, but the training that I provide is not an in-depth -- you know, it's not an advanced training. This is -- this is more like a basic sort of getting your feet wet kind of training, and then they get more involved training from ESR.

Q Okay. You also mentioned in that section of your report, section 4, that the software has been discussed at meetings of about a hundred STRmix stakeholders?

A Yes.

Q Now, those stakeholders are generally speaking users of the software that bought and paid for it, right?

A Yes.

Q And those individuals at that meeting, they, I understand by ESR's rules, don't include persons who are involved in the development of other programs of genotyping software aside from STRmix? Competitors if you will?

A Well, it's a meeting for STRmix users. I don't think that it would be a criteria that they would accept people who are not using STRmix.

Q Okay. Thank you.

Finally, I'd like to talk about section 5 of your report. You offer in that paragraph that you reviewed the electropherograms and other materials in this case, and that you agree with the analyst's decisions here. Bear with me. I'll be brief on this one, but if you can pull up government 7, please? And that'll be in your binder, too. If you can pull up the government's binder and go to 7? Can you identify that document for me, please?

A I am sorry?

Q Can you identify that document for me, please?

A Yes. This is government Exhibit No. 7. It's an electropherogram from -- well, it says LS 15-3777 STRmix.

Q Okay. You state specifically in section 5 of your report that you concur with her conclusion to omit the D8 locus due to oversaturation?

A Yes.

Q That's on page 5 of 6. Can you tell me at D8 what the highest RFU level is that you see there?

A So the highest peak it looks to me in this electropherogram is 23,821 RFU.

Q Are you aware that the Michigan State Police through their policy manual set their saturation threshold at 25,000 and in their validation study at 31,000?

A Not specifically aware.

Q Would that change your opinion about whether or not this locus was oversaturated knowing those were their protocol?

MR. PRESANT: Objection, Your Honor. The attorney for the Defendant should show the witness the document so he can --

MS. KLOET: He is looking at it on the screen.

MR. PRESANT: No. The protocol she is referring to about what their thresholds are. I mean, Ms. Smith testified last year about specifically these issues, and so she's asking the witness about policies that that witness hasn't seen and how to apply them to this document. She should show him that document.

THE COURT: Do you have the document?

MS. KLOET: Your Honor, it was admitted previously as government 11. I am happy to pull it up and I do have the page number.

THE COURT: Okay.

MS. KLOET: It was included in the exhibits that he reviewed. It's page 109. One moment, Your Honor. The one above it. No. That's right. That's right. Sorry. So I have highlighted a portion of this page here.

BY MR. KLOET:

Q Can you read the title and the first sentence there?

A So the title is STRmix eligibility. All available loci and alleles greater than or equal to the 250 RFU analytical threshold and below the maximum peak heights of 25,000 RFU's

should be utilized during the initial interpretation. It should be noted that peaks not represented by an allele artifact do not need to be included within the initial interpretation.

Q So isn't this saying that even if it's below -- well, if it's below 25,000 RFU, as long as it's greater than 250 it should be utilized during the initial interpretation? Isn't that what that first sentence says?

A This is what the first sentence is saying. And I would point out that this is during the initial interpretation of the electropherogram by the analyst before anything goes into STRmix. So after looking at the data, I guess there was -- yeah. Technically this is below the 25,000 RFU maximum peak height, but that was during the initial interpretation stage.

Q One moment. So I am showing you what was previously marked as government Exhibit 10. Do you recognize that?

A Yes.

Q What is that?

A That's the validation summary of STRmix.

Q And can you tell me where it says here what the saturation threshold is for the STRmix program? It may be reflected in at least in one spot on page twelve.

A Yes. This is after inspection of figure one we recommend a saturation threshold setting of 31,000 RFU.

Q Okay. So the 23,000 figure that you referenced on the

electropherogram, that's below the saturation threshold for the STRmix application, as well, right, at least as outlined in the validation summary?

A Yes.

Q In your opinion as a forensic biologist would it be advisable to rerun the sample to bring the peak level down to an RFU limit that doesn't exhibit that kind of oversaturation?

A Well, there is a give and take that goes into this thought process. So obviously when you have a low level contributor, the more DNA you can put into the reaction then there is a better potential that you will get a good idea of the peaks that are there in the profile. By decreasing the amount of DNA, rerunning it or reamplifying it at, you know, doing another reamplification at lower inputs you may lose more information. So there is this sort of balance between putting -- getting the sweet spot with ample amount of DNA without creating too many of these artifacts versus not enough DNA and having no information at all.

Q Would it surprise you if I told you that the policy manual that you were provided in preparing your report advises that the analyst do just that, rerun the sample?

A I would not be surprised. Sure.

Q Thank you. As long as we are talking about your review of the EPG in government 7, the electropherogram, if I can call your attention to locus D12? So seven alleles appear to be

present on that electropherogram at locus D12, correct?
A Seven are labeled.
Q Seven, I'm sorry?
A Seven peaks are labeled.
Q Okay. Thank you. Now, in operating under the assumption that each -- most people carry two alleles each, one from mom and one from dad, wouldn't the presence of seven alleles potentially suggest the presence of four contributors in this mixture?
A It's possible. But again, that is something that one would have to determine after an interpretation of the profile and I think is reasonable to assume that something like the 16 allele would be possibly stutter. You know, depending upon the locus here at D12, that one could determine that would be stutter product and not an authentic allele.
Q And just to recap, stutter is a by-product of the workup of the DNA?
A That's right. It's an artifact of the PCR process.
Q So not a true DNA --
A That's right.
Q You can put this -- put the electropherogram away much to everyone's relief I'm sure.

You testified earlier during our discussion, if you have known contributors that could be helpful for an analysis depending on the circumstances.

A That's right.
Q Okay. If the mixture might have the presence of a possible relative, would that be useful information for an analysis, as well?
A I mean, that probably would not be helpful at all as far as setting up your likelihood ratio whether you have a relative or not. It's really the number of contributors. But there is a calculation that can be performed and STRmix does perform that if you consider a relative as part of the mixture.
Q Can you tell me whether the Michigan State Police validation back in February of 2016 covered that scenario, whether potential or actual known relatives were in any of the mixtures they validated?
A Gosh. I would have to relook at their validation study. Off the top of my head -- I can't recall off the top of my head. It's been several weeks ago.
Q Okay. So you are not aware or you don't know right now?
A I don't know at this moment.
Q Okay. I want to ask you a few questions about how the Michigan State Police applied drop-in to STRmix. Can you describe for the Court what drop-in is in this context?
A A simple way to think about drop-in is it being a contamination event. So there is a difference between contamination in the classical sense is that in the laboratory we will run what we call negative controls. That's to make

sure that you have a sample where there is no DNA but it has all of the reactants, all of the materials that are in there, and you expect to see nothing. You expect that it goes through this PCR process but it doesn't generate any peaks.

Now, if -- if I were to go into the lab and start hacking and coughing over the PCR reaction, there is a chance that you may get a cell or two or three of my DNA get into that reaction and then you see this profile, this little minor contaminant profile in a negative reaction, negative control.

Now, that's what we call gross contamination where you may have a full profile or maybe a partial profile. What we mean by drop-in is generally one allele, a single allele that is foreign to the reaction. And again, that could be -- who knows where it comes from. It could be the guy at the factory who is making the buffer sneezes and now we've got parts of his DNA that's in the buffer and so when we go to do the reaction we see this one little peak show up.

Now, what distinguishes this from gross contamination is typically when you reamplify that reaction again it may be missing. It may not show up again. So it's a spurious sort of one time maybe one allele, maybe two at the most, but that's typically what we call drop-in.

Q Okay. In the STRmix program there are three kinds of preset values that have to be set for drop-in before the program is run on a sample, correct?

A To my knowledge. This is an area that I am really not familiar with, because at the University of North Texas we are not modeling for drop-in so I don't know much about the process, but I will agree.

Q Okay. Do your best. So one of those is drop-in frequency, and that is the rate of drop-in that's observed during the lab's internal validation, correct?

A Okay. Yes.

Q Okay. Another is the drop-in cap, and that is the maximum height of a peak that would be a proposed drop-in. This is as high as it can get before we are not going to consider it drop-in and instead consider it a true presence of an allele?

A That's right. That's usually done, like I said, you run a bunch of negative controls and you see what's the highest.

Q And the third value that would be set in terms of drop-in parameter, and I understand this is to be how STRmix assigns a probability of peak in drop-in based on peak height, analytical threshold and observed drop-in rate?

A Yes.

Q And drop-in frequencies can necessarily vary from lab to lab, right?

A It can.

Q Right. And the FBI's internal validation of STRmix they set a drop-in frequency of zero, didn't they?

A Yes.

Q And the New York City office of chief medical examiner, when they validated STRmix their drop-in rate was .0024. Does that sound about right?

A I am not familiar with their protocol but I don't know.

Q Would it surprise you if I told you that the District of Columbia, when they validated version 2.3 of STRmix, inserted a drop-in frequency of .0004545?

MR. PRESANT: Your Honor, I am going to object. The witness has testified that he is not familiar with these different drop-in rates so it sounds like Ms. Kloet is just testifying now to what she's found in other sources.

THE COURT: I think it's a fair question, Mr. Presant.

MS. KLOET: Your Honor, I do have those studies that I can present to the witness if you would like me to have him testify from the documents themselves.

THE COURT: If you think they are important to be in the record that is fine.

BY MS. KLOET:

Q Well, I'll give them to you for the ease of your own testimony. How is that?

A Thank you.

Q All right. Can you do your best to identify or describe the document that's on display?

MR. PRESANT: Your Honor, I haven't seen a copy of this document.

THE WITNESS: So this appears to be -- I'm sorry.

THE COURT: Go ahead.

MS. KLOET: Go ahead. You are fine.

THE WITNESS: This appears to be the internal validation of STRmix version 2.3 from the District of Columbia Department of Forensic Science.

BY MR. KLOET:

Q Can you -- can you look at page 21 of that document, please? And at the top of this page under 4.1.8 this discusses the phenomenon of allele drop-in, right?

A Yes.

Q What do they say was observed at the D.C. lab in this report?

A Under the section that says allele drop-in 4.1.8, drop-in has not been observed in DFS 28 cycle identifier plus profiles and therefore is not enabled within STRmix.

Q Okay. How about -- I'd asked you about New York City, I believe, and so I am pulling a document up now in relation to that. Can you do your best to identify this document?

MR. PRESANT: Your Honor, I also don't have a copy of this document.

THE WITNESS: So this is the forensic biology protocol for forensic STR analysis, the STRmix probabilistic genotyping software operating instruction. And at the very bottom it says New York City Office of Chief Medical Examiner.

BY MS. KLOET:

Q Thank you. Can you turn to page 34, please? Can you tell me what the lab setting for drop-in frequency was in New York City?

A So the drop-in frequency is 0.0024.

Q Thank you. So can you identify this document that's on display on your screen?

A This is the estimation of STRmix parameters for Palm Beach County Sheriff's Office.

Q Is there a date on that document?

A If there is it's hard to see. Looks like 5-30 maybe 2017.

Q Okay. Thank you. If you could please turn to page 6? I don't think that's the right page 6. I'm sorry. Now on display on your screen is page 6. And can you tell me what the drop-in frequency was for the Palm Beach County validation?

A It looks like 0.0112.

Q Okay. Thank you. If the user STRmix set a drop-in frequency of, say, .99, that frequency would affect the ability of STRmix to reliably interpret a DNA sample, right?

A I don't quite -- so you said if they set a frequency of .99. So 99 percent of the time you are going to have drop-in would that affect the reliability?

Q Of the result generated by STRmix, yes.

A I would suppose. I don't know. It's very hard to do these kinds of exercises without actually running the software to see

what the effect is.

Q So frankly, what that number would be doing is assigning too many true alleles as drop-in alleles, is that a fair characterization of what the drop-in frequency --

A So typically my experience is when you have to invoke drop-in to explain an allele, it typically has a deleterious effect on the likelihood ratio. It tends to significantly lower the likelihood ratio. In other words, it's more conservative to the person of interest which drop-in is invoked, but I would also caveat that with the fact that these parameters, I know you have listed at least three here, these are all coming from different kits in different labs under their conditions. So this is really a lab specific parameter here.

Q Okay.

A The one lab said they didn't observe drop-in. That was D.C. We haven't either at UNT, so we don't use that frequency at all.

Q Thank you. If you could pull up government's Exhibit 25 in one of the binders there? And I'd ask you to turn to page 2, which is at an angle. So I am calling out the bottom half of that page once you get there on your screen, as well.

A Okay.

Q Can you tell me or can you confirm for me that the drop-in frequency rate set for or set by MSP in this particular case

and inputted into STRmix was .3453?
A That's what it says.
Q You personally have never heard of that high of a drop-in rate, have you?
A I can't really -- have not talked to labs that much about drop-ins, so I don't know to be honest.
Q Is that a no that you don't personally know?
A No. I don't personally know.
Q Okay. A drop-in frequency of .3453, based on your prior testimony, essentially means that depending on the heights of the peaks being considered STRmix would be considering a probable of drop-in more than one in three observed opportunities?
A Well, this is not so much assigning but it's modeling. So I think there is a little bit of a difference there in exactly what you are saying, but these are what the values are. So I don't know much more than that.
Q Why -- when we talked about drop-in generally you characterize it as contamination. Why would Michigan State Police have such, for lack of a better descriptor, a dirty lab compared to some of these other labs that we went through?
A I don't think necessarily it's the product of being a dirty lab. I think, again, this is just a modeling thing that's happening in the software to explain potentially a spurious allele that may show up. And we have to remember as I

mentioned earlier in the day that the STR kits are much more sensitive than they used to be. We have now 20 loci that we are looking at instead of the 13. So we had this change in the STR kit chemistries and so forth that have made these kits much more sensitive. So I don't think it has necessarily anything to do with the cleanliness of the lab. It's the fact that out in the environment there may be other contaminating factors that one may see in evidence that's collected out in the environment.

Q Okay. But in any case when you say modeling, it's modeling that information, that's inserting information that's not necessarily there but probably simply --

A So yeah, in that Markov Chain Monte Carlo process that STRmix goes through it's doing a lot of asking potentially what if drop-in was now? What if it wasn't? So it's pulling from this sort of distribution to model that in its hypothetical answer. It may end up not modeling drop-in. It just depends. Like I said, it's kind of hard to draw a stiff conclusion based upon this theoretical number here unless you have actually run -- I'd like to run some samples to see what the effect is.

Q In real life testing where you don't have the known answer necessarily can a true likelihood ratio be knowable?

A There is no such thing as the true likelihood ratio for a crime scene sample where you don't know the contributors. I mean, we may have very good some cases where like we said the

sexual assault with the vaginal swab we can have very good confidence that we know one of the contributors there, but yeah, there is no such thing as a true likelihood ratio. This is a probability or a ratio of two probabilities.

MS. KLOET: Thank you, Dr. Coble. I have no further questions.

THE WITNESS: Thank you.

THE COURT: Dr. Coble, I just have one question and it's, maybe, and then you can go.

The development of probabilistic genotyping as you have testified to here today and spent so much of your professional life working on, is certainly intended to be and I think probably is an improvement on the ability of science to identify through DNA samples the individuals who contributed that sampling. What's the next best thing that's coming along? Is there anything out there that is now going to replace probabilistic genotyping?

THE WITNESS: No, ma'am. It's my opinion probabilistic genotyping is here to stay for today's technology and the future. So when we move to what we call next generation sequence, something where instead of looking at peaks we are actually going to sequence those peaks and get the actual A, T, C, and G's, we will be using probabilistic software to interpret those mixtures, too.

So I think this is really, I call it what -- it's not

unique to me, but a paradigm shift in the way we interpret evidence and I don't see that it's going to go away. In fact, there is a clammer. People are wanting the same kind of probabilistic genotyping software for Y STR mixtures, because you commonly get mixtures of men more than -- and like I said, in that sexual assault case you may get a couple of men, the husband and an unknown contributor, and those Y mixtures are just as horrible to interpret. And a probabilistic approach would be very welcome by the community at this point.

THE COURT: Great. Thank you, Dr. Coble. Your testimony has been most enlightening.

THE WITNESS: Thank you.

THE COURT: Okay. You may be excused.

(Witness excused, 2:05 p.m.)

THE COURT: And if nobody has any objection we're going to go right straight into -- right straight into Dr. Krane's testimony.

Dr. Krane, would you please come forward? I know you have been sitting back there very patiently.

DAN EDWARD KRANE, GOVERNMENT

having been first duly sworn, testified as follows:

(Witness sworn, 2:06 p.m.)

THE CLERK: Please be seated and state your full name for the record and spell your last name.

THE WITNESS: My name is Dan E, as in Edward, Krane.

That's spelled K-r-a-n-e.

THE COURT: Now, Mr. Presant, you deposed Dr. Krane, correct?

MR. PRESANT: That's correct, Your Honor.

THE COURT: Are you -- and I have not read the deposition. I don't know how far you got into of what you think you need from Dr. Krane's report and so forth, but are you satisfied with the questioning that you did there or would you like to start from scratch and go ahead right here?

MR. PRESANT: If I can take a third course, Your Honor? I don't think I need to start from scratch. I do have some followup questions but I am prepared to rely on the deposition record which has been filed with the Court for large portions of what I've already questioned him about. And I'll try to make my presentation here today more tailored to just a couple issues.

THE COURT: That's fine. You know, and I really do not mean to hurry you along. I realized we went a long way with Dr. Coble, but frankly, for my purposes it was necessary. And if that's -- if you've got questions for Dr. Krane that will further enlighten me about this technology then you take as much time as you need.

MR. PRESANT: Thank you, Your Honor. Your Honor, as I just mentioned, as you know, there has been some litigation over the government's view that Dr. Krane has a conflict of

interest or bias. I am just going to rely on the deposition transcript for that. I am not going to spend any time today on that unless the Court is interested in me developing that?

THE COURT: As you wish, Mr. Presant. I know that you do have some concerns in that regard. If you feel it needs to be further explored, that's fine. If you don't, that's fine as well.

MR. PRESANT: Thank you, Your Honor.

DIRECT EXAMINATION

BY MR. PRESANT:

Q Dr. Krane, I want to start with you this afternoon by talking about the analytical threshold and the stochastic threshold. Were you in the courtroom for all of Dr. Coble's testimony on those two topics?

A I was.

Q Do you take any issue with the way he described those two thresholds?

A I do not.

Q That's fast.

A I aim to please.

Q You also saw the government's Exhibits 33 through 36 regarding the record of external auditing both here in the courtroom today and at your deposition, right?

A I first saw them during the deposition. I don't think I have seen them in the courtroom today but I presume they are

the same as the attachments that you sent to me on Friday afternoon.

Q Are you satisfied that the external auditing done of the Michigan State Police's internal validation of STRmix and other internal validations relied upon in DNA mixture analysis by the Michigan State Police are the best we have in the forensic DNA community for external auditing of a lab like the Michigan State Police?

A I am afraid I may not have followed the question. It seems like there were a couple of threads weaved together.

Q Let me ask a better question. Based on the evidence of external auditing you have seen, would you expect to see any additional external auditing that has not been done by the Michigan State Police?

A No.

Q At your deposition we discussed this issue of determining the true number of contributors, correct?

A I recall discussions about the number of contributors, yes.

Q Would you summarize for the Court your opinion on whether the true number of contributors to an evidentiary sample of DNA can be -- can be determined with certainty?

A Well, you asked for a summary and I will summarize by saying that you could never determine with certainty the number of contributors to a questioned sample.

Q That's true for a single source sample or mixture, correct?

A It is.
Q So it's a matter of statistical certainty the number of contributors in a particular evidentiary sample?
A Did you say it's a matter of statistical certainty?
Q Yeah. It's -- you can have a degree of confidence in the number of contributors in a particular sample which I might call statistical certainty. You can have 95 percent confidence or 99 percent confidence, but you can't be a hundred percent confident in the number of contributors in a sample, is that fair?
A Generally. So what we are talking about here, if my recollection translated to about a half an hour of discussion that we had during the course of that deposition, and when you say statistical certainty, I would say I'd be more comfortable talking in terms of things like a 99 or a 95 percent confidence level. Certainly it's possible that you'd be able to evaluate a sample and say with 95 percent confidence this is a single sourced sample. There are ways by which that could be done.
Q What about a mixture? Can you determine with the 95 percent confidence that it's a three-person mixture?
A Theoretically. I am not aware of any generally accepted approach for establishing that type of estimate at this time.
Q Let's talk about the sample in this case. You are aware that Michigan State Police determined that it was likely a mixture of three individuals, correct?

A For the purposes of the STRmix analysis they treated it as if it was a three and only three-person mixture.
Q And you disagree with that?
A I am concerned about that. I think that's an overreach beyond what the data might support.
Q Do you think it's a four-person mixture?
A It could be.
Q Do you think it could be a five-person mixture?
A It could be.
Q Could it be a hundred person mixture?
A Much less likely, but yes, it could be.
Q So what would your 95 percent confidence level be in this case for the number of contributors in a sample? What would your range be?
A As I testified just a moment ago I am not aware of any generally accepted approach for establishing such a confidence interval, but I would add that I have been the lead author of -- the corresponding author of a study that demonstrated the first time to the forensic science community that there is a significant risk of underestimating the number of contributors using the approach that the Michigan State Police laboratory used in this case.
Q And what approach specifically is that?
A Essentially determining the number of alleles -- the locus that exhibited the largest number of alleles.

Q So at your deposition you agreed, though, that it's much more likely in this case for it to be a three or a four-person mixture than, say, a hundred person mixture, right?

A Yes.

Q And you also agreed that you didn't do any analysis in this case that would allow you to figure out what the 95 percent confidence interval would be, right?

A As I have said twice now I am not aware of any approach that would allow a reliable estimate to be made, and so no, I did not. During the deposition I think I suggested that there may have been some simulations that we could have done that might have helped shed some light on that issue, but I wasn't aware that that was something that the Court was interested in my opinion on, so I did not do them.

Q So it would be possible to figure out a 95 percent confidence interval? Simulations could be done?

A Well, we could do simulations that would help shed some light on that, but again, I am not aware of any generally accepted approach for attaching a confidence interval to such an estimate.

Q Now, you have also heard testimony today that if the -- and we covered this at your deposition, too, that if the number of contributors assumed by the analyst is incorrect, that tends to have a conservative or Defendant friendly impact on the likelihood ratio, correct?

A I have heard testimony and I have followed along on some of the publications that were being allowed to during that testimony, yes.

Q And do you have a different opinion about whether that's generally the case with STRmix?

A No. I do not. But I would emphasize the word tends. And Dr. Coble on a number of occasions used typically or generally to qualify it. It's not a certainty by any means.

Q And there are very few certainties in empirical science, correct?

A I suppose so.

Q And so examples given by Defense counsel earlier this morning about false-positives in studying breast cancer, correct, or testing a patient for breast cancer, do you remember those questions?

A Maybe I didn't hear the specific test. I remember Dr. Coble talking about strep throat tests.

Q I think it was in response to those, yes, sir.

A Okay.

Q So in the medical setting it's not uncommon for there to be false-positive or false-negatives for the tests administered, correct?

A Correct.

Q It's a matter of probability or accuracy of specificity of a particular test?

A It's certainly a very important consideration in any testing process, yes. And if I could add, there is a balance that gets struck. The efforts that you make to minimize the chance of false-negatives correspondingly increases the risk of false-positives and vice versa. There is a balance that needs to be struck. And people make -- need to make a deliberate decision about what their tolerance for false-negatives are, being mindful that that's going to have an impact on the risk of false-positives. I don't think that's an alien concept in a criminal courtroom. I have heard the suggestion it's better that 10 guilty men go free than one innocent man go to jail, and that's another manifestation of the same issue.

MR. PRESANT: May I approach, Your Honor?

THE COURT: Yes.

BY MR. PRESANT:

Q I am handing you a paper that hasn't been marked as an exhibit, but is entitled, uncertainty of the number of contributors for the European standard set of loci, and it's by James Curran and John Buckleton. Do you see that?

A Yes.

Q Are you familiar with this paper?

A Yes. I am. In fact, I will note that the first two references in the paper are to works on which I was the corresponding author.

Q And what's the general conclusion of this paper?

A Oh, it's essentially what we have been talking about a little bit today, and that is that typically underestimating the number of contributors does not have a significant impact on the likelihood ratios reported by testing software.

Q Now, at the end of your deposition, Dr. Krane, you testified that you really only had two criticisms of the forensic work done in this case, right, two and only two?

A I suggested I think my report ultimately could be categorized into two sets of concerns, yes.

Q And the first of those two criticisms was this issue with the coding standards, whether the software was up to par with IEEE best practices, right?

A I would have said that's the second but that is one of the two.

Q That's one of the two in no particular order?

A Right.

Q And the second criticism is whether the internal validation study set the outer bounds such that the case work done here was within those outer bounds, right?

A That's a fair characterization, yes.

Q And to drill down that a little further, it was really whether the minor contributor studied in the internal validation study was low enough and whether the experiments on those minor contributors were also done in conjunction with the amount of template DNA, right?

A I feel like we have accomplished something in the course of that six or seven hour deposition because I think at the onset you didn't have a clear understanding that I think you have parroted it back to me very nicely and I was delighted earlier when I heard you and Dr. Coble talking about how it's the two in combination that really need to be considered, not in isolation.

Q That's why we have depositions, of course, to make sure we can figure out the basis of opinions. And in your report it was really the work that was done by that conjunction. And I am looking for the sentence. Do you know where that sentence is in your report with the word and that we really honed in on?

A Well, I have a copy of my report. Let me take a look and see if I might be able to find it. Well, I don't know that this is the most on point instance of that particular operating, but at the top of the second page in the first full paragraph there, in the second line right after the ratio, there is an and that would have been an instance of the use of that and.

Q I think I found it. It's the bottom of page 4. There are two instances in your report and the sentence is the evidence sample in this case appears to fall outside of below the ranges of percent contribution and a quantity of template contributed for which the MSP laboratory has validated STRmix, correct?

A Yes.

Q In your deposition we agreed that you used the word appears here, and later in the report the word seems because you haven't seen data that showed the experiment was done both at that relative contribution of the minor contributor and at the amount of template for the minor contributor, correct?

A Yes. But I would refer to the language in the deposition -- not in the deposition so much as the report. I think the report is very carefully and tightly written in that regard. Yes.

Q So another way to put this is you agree that the internal validation study validated samples down below the seven percent contributor, and you also agree that it validated samples down to below those containing 49 picograms of DNA. Those were the numbers at issue here, right?

A So as I say in the report, I looked very carefully at the transcripts of the May deposition from last year and I saw nothing that speaks directly to that point. And I also looked very carefully, you know, extensive look at the validation summary. And while it was clear to me as I say in the report that there were at least a couple of instances where the lowest level contributor had contributed less than seven percent, and it was also clear that there were instances where the lowest contributor had contributed less than 49 picograms, it was not clear that both of those had happened at the same time. I did suggest in the report that there might be, as best as I could

tell from a very careful look at the validation summary, there may have been a few instances where both of those conditions were met. I suggested it might be as few as five to ten.

Q You acknowledged during the deposition that the Michigan State Police could address your concerns by providing additional data from the internal validation study, right?

A I think I did. I also recall talking about the possibility of addressing the concerns with an after-the-fact validation, where an experiment was deliberately set up to mimic those particular circumstances. There are some potential problems with that type of post hoc type of validation but it would be better than no efforts to do that at all.

Q So let's go to Exhibit 40, please. Have you reviewed government Exhibit 40?

A Will I find 40 in this?

Q You'll find it in here. It is also one of the attachments I gave you last week.

A Was it attachment 12?

Q I believe it was attachment 12. It was that letter from the Michigan State Police with supporting data.

A I have received that letter from you just after four o'clock on Friday of last week. Yes.

Q I think this was filed and sent to you on Wednesday, but I am sorry you didn't get it until Friday.

A I recall I received it at 4:13 p.m. on Friday.

Q That's a very good recollection. Very specific.
A It was notable.
Q Did this letter and the supporting data in government's Exhibit 40 address the criticism in your report of not seeing that experiment down to the lowest percent contributor and the lowest amount of template DNA that would support the case work done in this case?
A It's on point. It's helpful. I am afraid it doesn't quite touch at the core of the concern that I have, but it's -- we are in a better position with this information than we were without it. To some extent I think it does raise some new questions, as well.
Q Let's start with the data.
A That would be an excellent idea.
Q Page 3. And you understand these samples to be from what?
A These look as if they have come from adjudicated cases.
Q From the internal validation study?
A That apparently were included in the internal validation study, yes.
Q Okay. So for example, if we look at the second line, that's a seven percent contributor with calculated 14 picograms of DNA, right?
A That's what the table says, yes.
Q And the third line four percent and 10 picograms?
A Yes.

Q The seventh line, four percent and 28 picograms?
A Yes.
Q And next line, four percent and 28 picograms?
A Yes.
Q And the last line of the table five percent and 37 and-a-half picograms, right?
A Yes.
Q And you agree that the minor contributor at issue in the case work in this case is at seven percent and 49 picograms, right?
A Seven percent is what STRmix estimates is the most likely contribution from the lowest level contributor if it's a three-person mixture, and based on the testing laboratory's quantitation of the sample, seven percent of the tested DNA would have corresponded to 49 picograms.
Q So then if we look at those five lines of the table of the adjudicated cases, those are all instances where the internal validation study looked at cases with parameters that support the case work in this case, right?
A These are instances, five instances of analyses that were performed on samples that are outside of the range that would encompass a seven percent low level contributor at 49 picograms. They are outside of that range, which was essentially the essence of the concern that I was raising is that it didn't appear -- it wasn't obvious from the validation

summary that there were any samples that met those criteria.
Q And so this table in part satisfies that concern that you had?
A In part, yes.
Q Let's go to the next page. What do you understand to be depicted in this table?
A Well, as the title suggests, these are mixtures that were created within the laboratory, and here the table has been set up in such a way that there is a focus on the percent contribution of the lowest level contributor, and also the quantity of DNA that that lowest level contributor would have added to the mixture.
Q And so the second line shows a 4.7 percent lowest contributor with 47 picograms of DNA. The next line shows 3.2 percent with 32 picograms. Two lines down is 3.8 percent with 38 picograms, and then the last two lines, 4.3 percent with 43 picograms and 4.5 percent with 45 picograms, correct?
A That's what it says.
Q Once again, there are five instances of data, additional data that they provided you from the internal validation study that set an outer bound of what the lab was capable of doing that encompasses the work in this case, correct?
A I feel gratified that somebody was listening to the concern, because this is on point to that concern. Those are tests that were performed that fall outside of the range that

it was apparent was tested from the validation summary.

Q And so you said then you have more concerns even though these are 10 examples of experiments that suggest the work here was within the parameters of the Michigan State Police's validation study. What's left to be answered in your mind?

A Would it be possible for us to go back to the previous page?

Q Sure. There are a couple of things about this table that I think would bear further scrutiny, and I am thinking particularly about the second to last line and the first line where the third contributor, the lowest level contributor is contributing two or three picograms of template DNA. I don't know from this table what the likelihood ratios were for any of these samples, either on this screen or the one that we had just been talking about. I think that would be extremely important and helpful to know, in addition to what we are seeing here.

I know from the validation summary that there is a suggestion that there is a tendency for the likelihood ratios to be significant but less significant as you get less and less material. I specifically would like to know especially for samples like those that are by anyone's estimations very marginal samples what the false-positive and the false-negative rates are and what the likelihood ratios were for those particular samples. I am particularly interested in the two

that I just pointed to, the one where the contributors were two and three picograms. Because if STRmix was able to generate a likelihood ratio, a significant likelihood ratio as what's described in the validation summaries for samples where there is that little amount of template DNA, that would be significantly at odds with what's in the published literature about STRmix's behavior for such low level samples.

Q Did you read the paragraph at the bottom of the table if we can scroll down?

A I did.

Q So you understand these to be adjudicated cases, correct?

A I do.

Q And so the true nature of the sample is unknown, of course, because it was recovered from the world? It's an evidentiary sample, right?

A Yes.

Q And so therefore, we don't necessarily know or we don't know exactly who was in the mixture or who was not, right?

A I suppose. Yes.

Q So what's the purpose, then, of looking into adjudicated cases in a validation study?

A To see if you get generally consistent results as what you had gotten during the original investigation before a tool was available.

Q Right. So what about the next page? Are there any other

experiments you would like to see on the next page?

A So for the page that we have just been talking about with the two and the three picograms, I think there is concerns that you have just been touching on with respect to adjudicated case work for validation studies. And so if we set those aside, and I think a reasonable case could be made that we shouldn't be talking too seriously about those, the ones on this page that we are looking at right now, these are actually controlled experiments where the known contributors were known. And in these instances, again, we are seeing some data that suggests that the laboratory has evaluated samples that meet those criteria. I believe five was the number that we have been talking about. Both low level and low amount of template.

Again, I think it would be extremely helpful for these samples to see the actual test results. I personally would like to see the electropherograms, but at the very least in the context of this discussion I think it would be very important to see another column that gave the likelihood ratios that STRmix reported, and if possible, something about the false-positive and the false-negative rates associated with those types of samples.

Q Safe to say you'd always like to see a little bit more data whatever the experiment is?

A Well, that's safe to say, but I think that's glossing over what I think is a fundamental concern about some missing

information from this table. Because in the absence of that information, all we have to work with is a superficial suggestion in the validation summary that the likelihood ratios were significant. And again, maybe it's because I have lived for some time in Missouri, I'd like to see what the underlying basis for that conclusion is. Really when you say significant are you meaning the same thing that I am? I think in this context that might be especially important because again, the crux here is I want to know, and I think the Court needs to know what are the limits beyond which we should be suspect of STRmix results? And really, you know, right now it's about me and the Court, but I think ultimately we want the analysts for the Michigan State Police to know where it is that they should proceed with caution, and that's how they would get that kind of information.

MR. PRESANT: Your Honor, the government offers Exhibit 40 again.

THE COURT: Ms. Kloet, have you had any opportunity to further evaluate government 40?

MS. KLOET: I have, Your Honor. And again, the genesis of my objection is that this appeared to be -- it's a letter directed to the prosecutor in this case and appeared to be a direct attempt to form essentially an addendum to the validation summary that was performed in 2016. I think, however though, my concerns end from Dr. Krane's ability to

address it properly on such a short timeline. I think that his testimony indicates that he is able to do so and I'll withdraw my objection.

THE COURT: Thank you. It's admitted.

MR. PRESANT: Thank you, Your Honor.

BY MR. PRESANT:

Q So Dr. Krane, stepping aside from Exhibit 40, I want to talk a little bit about other studies that have been done on STRmix with respect to low level contributors. And you probably heard Dr. Coble testify already today about the difference between kind of uninformative data and data that isn't reliable at low templates or very low contributors. Do you recall that?

A In the context of talking about peak heights relative to the analytical threshold?

Q No. I think it was later on. It was specific with respect to the issue of the number of contributors. Right. Forget it. Let me just start over. Are you familiar with the studies that have been done on STRmix by increasing the number of contributors by one?

A I am aware of such studies, yes.

Q And don't you agree that when you tell STRmix there is actually one more contributor than there is, that's in essence simulating a very low level contributor? STRmix is actually pretending like there is a contributor that's very close to

zero?

A I think there are better ways to simulate a low level contributor than by artificially overestimating the number of contributors, but yes, that is a way that you could simulate overestimating the number of contributors.

Q And if STRmix, when it overestimates the number of contributors, is actually simulating a very low level contributor, that in a way is suggesting that it's testing down to a contributor at effectively zero percent of the mixture, right?

A Again, there are better ways to test down. The behavior for a very, very low level contributor, zero, one or two percent, but in some sense overestimating the number of contributors does get us some insights into STRmix's behavior in those circumstances.

Q And when there is a very low amount of DNA involved in the mixture, isn't it also the case that STRmix will tend to a likelihood ratio of one as in as you decrease the amount of DNA available for STRmix to analyze you are going to get closer and closer to an informative likelihood ratio that has a likelihood ratio of one? Do you agree with that?

A Yes.

Q And so isn't that also another way of saying that STRmix has shown that it's able to analyze DNA down to very low template or very low percentage of contributors because the

output of STRmix is going to be uninformative?
A I don't know that we have looked carefully enough, including the papers that you are alluding to, to STRmix's behavior for such very low mixture ratios and quantities of template DNA. You might recall earlier looking at what were described as violin plots. If you look carefully at those violin plots you'll see that in the zero to one range there is quite a bit of overlap between known non-contributors and known contributors in terms of the likelihood ratios that are being generated. And again, that's the concern that we start to have where at those levels you might be getting indications of false-positives and false-negatives at unacceptably high rates for either or both.
Q Let's go to government's Exhibit 5, please. What's this document, Dr. Krane?
A Excuse me?
Q What is this document?
A Its title is, Internal Validation of STRmix For Interpretation of Single Source and Mixed Profiles. It's a paper that was published in the Forensic Science International Genetics journal.
Q Can we go to page 13 of the exhibit, which is page twelve of the article? And let's scroll down to this sentence beginning with, where profiles exhibit stochastic effects. And I'll just read it. Where profiles exhibit stochastic effects

in allele dropout, particularly at very low --

THE COURT: You're going awfully fast, Mr. Presant.

MR. PRESANT: Thank you, Your Honor. I always forget, So I can use as many reminders as the Court needs to give me.

BY MR. PRESANT:

Q Where profiles exhibit stochastic effects in allele drop-out, particularly at very low template where few or no obligat alleles for a given contributor are detected, the LR for false contributors as well as true contributors tends to spread slightly above and below one. I read that correctly?

A You have.

Q Can you put that in laymen's terms for us?

A Maybe not, but before when I was talking about the violin plots I suggested that if you looked carefully you could see that there was a significant overlap between the spread for known non-contributors and the spread for known contributors. That's exactly what this sentence is talking about, and that is that for these very low level samples, when the likelihood ratios are small, in the ballpark of one, there is a significant risk of saying that somebody we know was not a contributor to the mixture appears to have been more likely than not to have been a contributor to the mixture.

Q The work being done in that answer right there is when we are close to one?

A Yes.

Q Right. When we get further away from one we can be more confident that those two types of error, type one or type two error, are not occurring, correct?
A Yes.
Q So let's turn to the second primary criticism that you have of the work done in this case, and this is the --
A Second category of criticism.
Q Second category?
A All right.
Q That's the coding issue, right?
A More or less, yes.
Q More or less.
A It pertains to coding and software engineering issues.
Q Pertains to coding and software engineering. First of all, Dr. Krane, you have never used STRmix personally, right?
A STRmix has been available within forensic bioinformatics on a trial basis and I looked over the shoulder of people who were using it at the time, but I have not used it for forensic case work myself. No.
Q You have never personally reviewed STRmix's source code?
A I have not sat at the computer terminals as the course code was being reviewed, but I have been a party to nondisclosure agreements and then resultant discussions about source code reviews.
Q Someone who works for you has been retained by the defense

in this case. Nathaniel Adams is the person who has done the actual code review, right?

A Yes.

Q Is it fair to say everything that you know about STRmix's source code has been information that's been conveyed to you by Mr. Adams?

A I think that's fair. Yes. Certainly the overwhelming majority of what I would know.

Q Mr. Adams has only been partially willing to discuss those code reviews in open court, right?

A I read his transcript from the May 2018 Daubert hearing. That's correct.

Q Now, you have produced at least two pieces of software recovered in your deposition, right?

A I have been involved in the development of at least two programs, yes.

Q That's GenoStat and GenoFiler?

A Yes.

Q And you agreed and you still agree that neither of those pieces of software is compliant with IEEE standards?

A Correct.

Q And you said that was because the software wasn't sophisticated enough to be subject to IEEE standards?

A That's a fair characterization, sure.

Q So you have never been involved in a piece of software like

STRmix or any other piece of software that is sophisticated enough to be subject to IEEE standards?

A Yes.

Q You have never been involved in the development of such a piece of software?

A That's correct.

Q Mr. Adams hasn't either, correct?

A Not to my knowledge.

Q I am correct as far as your knowledge goes?

A You are correct as far as I know.

Q So would you consider yourself an expert in software development?

A I suppose it depends on how you define expert. I do have a courtesy appointment in a computer science department. I have spoken with people who I think anyone would agree is an expert. I think I probably have more insights into software development than the average person walking down the street, but there are many, many people who are more expert than me in that particular area.

Q So when you were deposed I asked you are you familiar with agile method of software method or the waterfall method of software development and you said you didn't feel comfortable testifying about what those methods were, right?

A I remember those answers and questions, yes.

Q Do you feel comfortable testifying about those methods of

software development today?
A No.
Q And I also asked you, much like with the issues for internal validation, if we are to put it to you, how could ESR and STRmix address your criticisms of the code development process and how the code is written for the various searches of STRmix? And you said that you would rather defer to someone with more expertise on how these things should be done, right?
A That seems like a very reasonable answer to such a question. Yes.
Q I think it is.
A Thank you.
Q And so sitting here today you don't really know how the code should be changed in order to address the various criticisms that Mr. Adams raised?
A Well, I think there are some things that would clearly help address those concerns that Nathan raised, things like establishing performance parameters, but in terms of specific changes to the code, no, I wouldn't be able to speak to that at all.
Q In fact, you also acknowledge that IEEE doesn't even require its own standards to be met. They say they are simply advisory and there are other methods by which software could be appropriately developed in compliance with other standards even if they don't comply with IEEE, right?

A Just as with SWGDAM, IEEE is making recommendations. There is no body that enforces that those recommendations be followed.

Q And neither you nor Mr. Adams has determined an actual error in the code or problem with the code that had a functional or operational impact on the likelihood ratio calculated in this case, correct?

A That would be a very unrealistic expectation finding such an error given the nature of the source code reviews that Nathan has been involved with.

Q Realistic or unrealistic, it hasn't been found, right, such an error?

A That's not -- correct.

Q I think you combined an answer of it's not and correct. And I think you were just saying correct, but I want to make sure the record is clear that that assertion was correct, no error has been found, right?

A Right.

Q Otherwise the record says it's not correct and everyone is wondering why not.

A I appreciate that.

Q Thank you for the clarification. So did you review government's Exhibit 18 in preparing your report?

A If it was included in the materials that were provided to me a few months ago, yes.

Q And 18 was basically a response to Exhibit 17, which was Mr. Adams's declaration of his case, right?
A Yes.
Q Point by point response to the criticisms that Mr. Adams developed, right?
A Yes.
Q Your report that you filed in this case doesn't address Exhibit 18 with any specificity, right?
A That's right.
Q And Mr. Adams also hasn't offered a response to Exhibit 18 in this litigation so far, right?
A Not that I know of.
Q And so if 17 is Mr. Adams's list of everything that's wrong with the code in this case, and Dr. Buckleton has responded in Exhibit 18 to each of those issues, no one has pointed out any problems with the analysis that Dr. Buckleton did, right?
A Did you say these analyses that Dr. Buckleton did?
Q The analyses he did of Mr. Adams's declaration.
A Not that I am aware of.
Q Is there anything you'd like to say now about 18, things Dr. Buckleton got wrong?
A It seems to me that falls outside the scope of what it is that I was asked by the Court to address in my report and that's what I have come prepared to speak to today, and so I think the short answer to your question is no.

Q You also acknowledged at your deposition that you were very -- it would be bad for your business if you came in court today and undermined what Mr. Adams said, right?
A I remember questions along those lines and I think my answer was more nuanced than what you've just suggested but --
Q I can try to find it for you.
A I think it's fairly obvious that if I were to contradict one of -- the work of one of my consulting company's key employees, that would -- it's hard to imagine that would not be bad for business.
Q I asked you a question would it have been bad for your business if Mr. Adams reached one conclusion in this case and you reached different conclusions that contradicted it? You answered, most likely, yes.
THE COURT: That's exactly what he just said.
MR. PRESANT: Yeah. I want to make sure I wasn't mischaracterizing what you said there at all.
THE WITNESS: Is that a question?
MR. PRESANT: If it was I'll withdraw it.
BY MR. PRESANT:
Q Okay. The last thing I want to talk about in your report is you touch on this issue with aviation software, right?
A I did mention some aviation software at the very end, yes.
Q And the point is similar to the point Ms. Kloet made with respect to various medical testing procedures is that when

important things in society are at stake, people's health, people's lives, people's freedom, that if there is errors in scientific processes that bad because bad things can happen and in the instance of aviation software it's that the plane can crash, right?

A Yes.

Q And you also testified, not only did you tell us but you testified that you got in a plane after your deposition a couple weeks ago, right?

A I made it to the airport with 40 minutes to spare.

Q And you got on the plane, right?

A I did.

Q You fly a lot for work, correct?

A More than most. Yes.

Q And you testified that you don't know how many pieces of software were run on a typical airplane, right?

A That's what I testified. Yes.

Q And you don't, right?

A Then or now.

Q Do you know how many of those software programs that run in an airplane are compliant with IEEE standards?

A I do not know the specific number, no, or a fraction.

Q But you still got on the plane after the deposition, right?

A I did.

MR. PRESANT: Nothing further. Thank you, Your Honor.

THE COURT: Thank you.

Ms. Kloet?

MS. KLOET: Thank you, Your Honor.

THE WITNESS: Would it be out of line for me to ask, Mr. Presant, at the deposition there was -- it was understood that I'd get a copy of the transcript of my deposition. I haven't received one.

MR. PRESANT: That was e-mailed to you in the batch of e-mails last week, but if you don't have it when you go look for it let me know and we'll make sure you get a copy.

THE WITNESS: Very good. Thank you.

CROSS EXAMINATION

BY MR. KLOET:

Q Good afternoon, Dr. Krane.

A Good afternoon.

Q Thanks for sticking with us. I am going to go through your report the same way I did with Dr. Coble this morning. It'll take a little bit less time due to the extensive testimony we've had so far.

The internal validation that Michigan State Police completed, that required the use of other equipment or software, correct?

A As part of the validation, yes.

Q Okay. One of those would be the kit that Dr. Coble testified to which I believe in this case was the PowerPlex

Fusion kit, correct?

A Correct.

Q Do you know when the validation on that kit was completed by Michigan State Police?

A As I am speaking to you now I don't, but I recall seeing some documents that gave that specific information at the very least during the course of my deposition two weeks ago.

Q I'll try to make it easy for you. If you turn to government's Exhibit 32, is that what you recall having been presented with?

A I have it. All right. I am damaging your binder but I have Exhibit 32.

Q Thank you. Can you describe that document, please?

A It's titled validation summary, validation of the PowerPlex Fusion STR chemistry kit.

Q So this is the kit that would be utilized at some point in the process prior to the employment of the STRmix software, correct?

A Yes.

Q Can you tell me, turn to page 2, please, when this kit was validated?

A It's -- this validation study is dated 2-3-14.

Q Have there been kits, whether PowerPlex Fusion or other brands, released since 2014?

A Yes.

Q Another piece of equipment or software that is utilized in DNA analysis prior to the deployment of STRmix would be a genetic analyzer software such as GeneMapper ID-X, correct?
A Yes.
Q Do you believe that version of GeneMapper ID-X was validated by Michigan State Police?
A I do not.
Q Can you turn to Exhibit 31 from the government?
A I am with you at 31. It appears it's the version 1.4.
Q Just to recap your testimony is the validation summary shows that the version of the analyzer that was validated by MSP was GM ID-X versus 1.4, correct?
A Correct.
Q And when was that validation completed, if you turn to page 2?
A The date on the document is December 2nd, 2014.
Q To your knowledge have there been more recent or updated genetic analyzer programs released since 2014?
A I believe that there have been, yes.
Q Okay. I'd like you to turn to the government's Exhibit 40. This is a letter that you were just discussing with Mr. Presant.
A I am at 40.
Q Thank you. Turning to page 3, where the chart is on an angle there, does this chart indicate to you that a particular

sample was run more than once to determine what likelihood ratios were generated?

A There are several items that have the same description. That might mean that they are the same sample that was run multiple times, but I can't be certain of that.

Q Okay. If we look at, for instance, the revolver?

A Yes.

Q And actually, let's take the one right above it, swab from H&R 22. This purports to show that third contributor's contribution was two picograms, correct?

A That's my understanding of the table, yes.

Q Does it indicate in this chart or anywhere else in this particular exhibit that a likelihood ratio is generated for that particular sample and then a second one was generated to see if they were near or close to one another?

A What was the last part of the question?

Q Whether or not -- does this chart show that whether or not a likelihood ratio is generated for that particular sample more than once, more than one likelihood ratio was generated?

A I don't see any indication that it was analyzed more than once.

THE COURT: Can I just interrupt one second?

MS. KLOET: Sure.

THE COURT: When you are talking about running more than one test, are you using the same DNA each time? It does

not get destroyed somehow in the process?

THE WITNESS: There are a bunch of different layers to the answer to your question. The PCR amplification process that you have heard testimony about, including by Dr. Coble earlier today, is destructive. So in the process of amplifying the DNA from a sample, that sample is destroyed. But the amplified DNA could be run through a genetic analyzer multiple times. And what gets run -- what comes out of a genetic analyzer would be submitted to STRmix multiple times.

THE COURT: Okay. I understand.

MS. KLOET: Thank you.

BY MR. KLOET:

Q Generally speaking with respect to this letter to Mr. Presant from the Michigan State Police lab dated last Wednesday I believe, do you have any concerns that the information contained in this letter was not contained in the validation summary that was issued in 2016 by Michigan State Police?

A Yes.

Q Can you describe those concerns for me, please?

A Again, I spent a fairly good amount of time looking at the validation summary that was prepared by the Michigan State Police. My report summarizes as best as I could glean from that fairly careful look what had been evaluated by the Michigan State Police. This information is not contained in

the validation summary. That's concerning to me not because I think that it's been fabricated or made up, but because I think it would have been very helpful to people who were reading the validation summary. I think the questions that I was pointing to are very reasonable and very appropriate questions and I would have hoped that a validation summary would have provided the information that would have answered those reasonable and appropriate questions.

So another concern that I have is that the validation summary and the validation study itself ultimately is there to provide guidance to analysts in the use of a new methodology, STRmix. If this information is not within the validation summary it can't make its way into the protocols, the interpretation guidelines for the laboratory, and it can't provide guidance to analysts, and the analysts then are not getting guidance on what I would suggest is perhaps one of the most important questions that they will encounter, which is at what point they should not be relying upon STRmix to help them in their work. And so again, those are concerns that I have.

You heard me in my answer to Mr. Presant, I have additional concerns about the suggestion that you might be able to get reliable likelihood ratios and output from STRmix from samples that are derived from as little as two picograms of DNA or three picograms. I think that finding by itself is worthy of careful evaluation just because it is at odds with what has

been in the published literature about where it is one might be able to get useful information if those analyses get borne out by some scrutiny, a look at the electropherograms, a look at the likelihood ratios in the STRmix output. Then I think there might be some important news to share with the forensic science community about capabilities that STRmix has that have heretofore not been appreciated.

So again there is a suite of concerns that I have. Again, as I said before, I feel gratified in seeing this letter that somebody paid attention to my report, and we are better with this information than we were without it, with this addendum in some sense than we were without it, but I don't think it quite addresses the crux of my concern with the scope of the validation study that the Michigan State Police seems to have conducted.

Q Thank you. And I'd like to call your attention to government Exhibit 10.

A I see it on the screen.

Q Okay. Can you identify it from its cover page?

A This is the validation summary for the STRmix PowerPlex Fusion test kit.

Q Okay. Before we delve into this particular exhibit, can you explain to me what you understand the purpose of an internal validation study to be? What some of the most important objectives are?

A I think there are essentially two categories of objectives for internal validation. One is to demonstrate that a particular methodology or approach or tool generates results that are consistent with what the proponents of the tool or methodology suggest could be obtained, right? So essentially to confirm that the developmental validation is consistent with what it is that the testing laboratory gets in their own hands.

But the other category is that an internal validation study should establish limits that give guidance to analysts about how and when to use this methodology and when, perhaps more importantly when not to use a methodology.

Q Can you tell me if the Michigan State Police validation summary of STRmix indicates that Michigan State Police itself determined that a mixture in their testing or validation process was too complex to analyze or when they got an incorrect run lab result in their estimation?

A There is very little guidance in the Michigan State Police standard operating procedures about, for analysts regarding when and how to use STRmix. There is some. There is a few words that say that if a mixture is too complex that analysts can choose to not use STRmix. And it's in the context of talking about the number of contributors. And it's very clear that the internal validation study only looked at two, three and four-person mixtures. And so I think it's fair to say that the SOP's for the State Police laboratory are suggesting that

if it appears as if you are working with a five or a six or more person contributor mixture that STRmix would not be appropriate.

Q All right. I'd like you to turn to page 43 of the validation summary. You mentioned a number of contributors. From this validation summary does it show that Michigan State Police took a known four-person mixture and attempted to evaluate it with an incorrect number of contributors?

A Well, I am reading from page 43, and in the middle of the page is a paragraph that says, four-person mixtures were not evaluated with the incorrect number of contributors because studies have already shown that STRmix will provide an error if the number of contributors is underestimated, and we are not validating five-person mixtures.

Q Is that a determination that MSP made on their own or was that based on the research of others?

A It's consistent with what has been published about STRmix. I don't know what the basis for the Michigan State Police determination was.

Q All right. I am going to -- are you familiar with the Alladios article that Dr. Coble testified to?

A Yes. I was provided a copy of it during my deposition two weeks ago.

Q Okay. Have you had a chance to read it since your deposition two weeks ago?

A I suppose the truthful answer is yes, I have had a chance, but I haven't taken advantage of the opportunity.

Q Well, do you agree with some of the recommendations that were made in that article that Dr. Coble was reading into the record, namely that the authors advised that using extreme caution with fully continuous software on low template DNA samples? Do you agree with that recommendation?

A Absolutely. And I would have agreed with that when I was first presented it two weeks ago. I noticed that specific caution at that time, as well.

Q And do you agree with the author's recommendation that or indication I guess of intent that further studies will be performed in order to combine the likelihood ratios results provided by different software algorithms using different interpretation waves? I guess my question is do you agree that's a good idea?

A I'd like to reserve judgment whether or not it's a good idea. It's an interesting idea. I liken it to what we see in the news about polls for presidential candidates. How there may be 20 different polls that are available, just as we have heard from Dr. Coble there may be a dozen or more probabilistic genotyping programs. Each one gives a different result. There are suggestions that the average of the presidential polls gives you the best insight in terms of the nature. And in that same spirit conceivably the average of the output from a number

of different probabilistic genotyping approaches might give you a better answer than any one by itself. Again, I think ultimately it's an interesting idea but one that will probably need to be borne out.

Q Thank you. I am going to move to section 2 of your report which discusses peer review. Now, I believe on page 3 of that report you state, virtually no publications are truly independent as it relates to STRmix. I think that was your statement. What are the implications of that to you from your perspective as an academic and as a scientist?

A Well, as I say in my report, there is unquestionably a value that is associated with extensive independent peer review. And that value can't be fully realized unless and until those types of independent validations are performed.

Q Did you have an opportunity to read Dr. Coble's report submitted to the court?

A I did.

Q He cites as evidence of peer review the internal validation article. Pardon me. Do you agree with his citation of that as evidence of independent peer reviewed literature?

A It's not in this part of my report. I think elsewhere in the report I point to the fact that proponents of STRmix do point to that in May of 2018 apparently there were 30 or so laboratories that adopted the use of STRmix, and proponents point to that as an indication of general acceptance and a

somewhat at least independent validation of STRmix.

Q And so your testimony was that proponents point to that. What about you, Dr. Krane, do you think that's sufficient evidence of a peer reviewed publication?

A Well, it's not -- it wouldn't by any venture be construed as being peer reviewed publications.

Q Why is that?

A Well, the peer review process is a fairly formal, broadly understood process where a scientist conducts an investigation, describes their results in a written report, submits it to a journal such as the International Forensic Science International Genetics, in which Dr. Coble is a member of the editorial board. The editorial board then elicits the opinion from typically two or three or four independent scientists to evaluate the report that has been submitted for publication. Those are typically anonymous peer reviewers that provide feedback to the editors, and in turn, often that feedback is shared with the author or authors to help them improve the manuscript. And it's only after that process has been completed to the satisfaction of the authors, the editors and usually the reviewers that an article gets published. That peer review involves independent experts typically anonymously evaluating a work.

Again, a laboratory validation study I don't think anyone would suggest is in itself a peer reviewed valid

process. It's an internal validation study. It's a kicking the tires on the car that you are thinking about buying. It's not publishing something that others might attach significance to.

Q And I'd like to move onto error rates and standards, section three of your report. There are several lab specific parameters and/or choices that analysts are faced when mixture interpretation takes place and when STRmix is utilized, is that fair to say?

A Yes.

Q I'd like to ask you about some of those decisions and how STRmix accounts for them and their potential impact. We heard testimony about drop-out and we heard significant explanation about what that means. Essentially my understanding is that's an artifact that may be caused in copying or amplifying the DNA, is that correct?

A Yes.

Q Okay. Can the phenomenon of drop-out affect an analyst's interpretation as to the estimate of number of contributors potentially?

A Absolutely.

Q Can it affect the analyst's interpretation as to certain allele calls potentially?

A Absolutely. And with respect to the number of contributors let me add that the error that drop-out might include would

only lead to underestimation of the number of contributors. It wouldn't result in an increase in the number of contributors that are estimated.

Q To the best of your knowledge, what does STRmix attempt to do with respect to that phenomenon?

A It models it.

Q What does modeling mean in lay person speak?

A STRmix takes into account a number of features of the data, the electropherograms, the graphs that get generated during DNA testing, the heights of the peaks for instance, and as you heard Dr. Coble testifying about an analytical threshold and stochastic threshold. STRmix doesn't use a stochastic threshold. It does use an analytical threshold. But instead of a stochastic threshold it says, gee, I've got a peak that's somewhere around here above the analytical threshold but it's not really tall compared to the baseline. Given its height there is a certain chance a probability that it has another peak that came with it from an individual who contributed two peaks instead of just one. And there is a chance that the other peak usually referred to as the sister peak or the sister allele has failed to be detected, meaning that it didn't rise above the analytical threshold. And so STRmix uses things like the heights of the peaks, the presence of stutter peaks nearby to help give it some indication as to what the relative chances that drop-out has occurred for any given peak that might be

considered.
Q So STRmix effectively inserts information that it thinks probably should have been there but wasn't actually is, is that --
A That's one way to put it, yes. It's considering the possibility that information should have been detected that failed to be detected due to sampling problems, stochastic effects.
Q Thank you. The next phenomenon I'd like to discuss we've talked about a little bit, too, stutter. And to simplify, stutter tends to suggest the presence of an allele that's not actually there. Is that a fair description of what that means?
A Stutter can appear to be an allele. It's an artifact that can appear to be an appeal that wasn't actually present in the underlying sample.
Q Okay. And there are two types of stutter, forward and backwards, correct?
A There are at least two types, yes, forward and backwards. There is double backwards, as well.
Q Okay. Can the phenomenon of stutter potentially affect the analyst's interpretation of allele calls?
A Yes.
Q How about the analyst's estimation of number of contributors, potentially?
A Yes.

Q What does STRmix do about that?
A Well, STRmix will model the possibility that a piece of information its been fed isn't really an allele but might be a stutter artifact.
Q And isn't it true that version 2.307 used by MSP in this case did not account for forward stutter?
A That's correct.
Q The third phenomenon I'd like to discuss is drop-in, and we had some testimony early this afternoon about that. That is essentially contamination, correct?
A That's a very simple way to put it. Yes.
Q All right. Does the presence of contamination potentially affect the analyst's ability to correctly interpret the electropherogram in a given case?
A Of course.
Q What does STRmix do about drop-in and the potential for drop-in, insofar as you are aware?
A Well, STRmix is capable of modeling drop-in to help it explain test results if it sees a peak that is -- for any given peak that it evaluates it contemplates in some computational sense the possibility that it wasn't really part of the underlying sample but is there because of this drop-in phenomenon.
Q You heard Dr. Coble testify earlier as he was reviewing the STRmix reports generated in this case that the Michigan State

Police drop-in frequency was .345, something along those lines. What does that mean to you?

A Well, what that means is that STRmix has given a fair degree of latitude for any given peak to consider that maybe in these circumstances that it is within this laboratory STRmix is given a fair degree of latitude that for any given peak it could explain it as being due to contamination as opposed to actually being associated with the underlying sample.

Q The fourth phenomenon I'd like to discuss with you is masking. Can you describe to the Court in the context of electropherograms?

A I actually heard Dr. Coble speak to this without putting those words to it. I think he suggested that his genotyping to the THO1 locus may be a 6/9.3 on the electropherogram. On the graph there would be two distinct peaks at that locus for him, a 6 and a 9.3. But if instead he was not a 6/9.3 but a 6/6, which is something he suggested might be the case, the two sixes would be sitting on top of each other. There would be an expectation that the two would stack. That they would add each other's heights. You'd have two separate peaks, but because they were all at one spot that peak would be proportionately higher than if they had been distributed across two separate peaks.

Q I understand. Might the phenomenon of masking affect the estimate as to number of contributors in a particular analysis?

A Absolutely. Again, only leading to underestimates of the number of contributors. To the extent to which masking or stacking is in play, that will exacerbate the problem of determining the number of contributors to a mixture by -- and the problem here being specifically leads to an increased risk of underestimation of the number of contributors.

Q Thank you. And the last biological question I have for you I hope isn't necessarily a phenomenon but a concept. What is pairing? What is allele pairing?

A Let's go back to Dr. Coble's THO1 DNA profile again. Hypothetically, if he is a 6 and a 9.3 they are a pair. He suggested his mother gave him one and his father would have given him the other. There would be an expectation that all of the nucleated vessels in his body would have one copy of the chromosome that he got from his mother and one copy of the chromosome that he got from his father. They would be a pair.

In electropherogram terms when we are looking at those peaks, the heights of the peaks are generally proportional to the amount of DNA that was present in the underlying sample.

For Dr. Coble, if he is a 6/9.3, for every 6 allele copy of that instruction there should also be a 9.3. They should be present in equal amounts. They should give rise to peaks that are roughly the same height. And so they are a pair. And we can see some evidence of that pair from the similarity of the heights of the peaks on an electropherogram.

Q So I think to summarize your testimony you can see evidence of a pair at a particular locus, is that correct, depending on the amounts?

A You can see indications that one allele is associated with another on the basis of its height. For a two-person mixture if you have a major contributor you might see two tall peaks. In a minor contributor might have two small peaks and you compare them with each other on the basis of their heights.

Q You don't know for certain that those alleles pair up? There is evidence suggesting as much, correct?

A You wouldn't know with certainty, and you'd have to be concerned that maybe you could make a mistake about the number of contributors. If you go back to my specific example, two tall peaks and two small peaks, that could be from one person who is given both the tall peaks and two other people who have given two copies of each of the small peaks. It could also be an instance where you have the two tall peaks are masking the contribution from another minor contributor and the minor contributor adds a little bit of height to one of the peaks but not so much that you say that it's not paired with the other peak and you have missed that third contributor entirely because the major contributor is masking a minor contributor's contribution.

So there is lots of problems. And the larger the number of contributors that you are contemplating the more

difficult the interpretation of a mixture becomes, which is ultimately one of the reasons that STRmix is generally used for two, three or four-person mixtures and relatively few laboratories are exploring the possibility of five-person mixtures. And there are none to my knowledge that are exploring it for six-person mixtures. Even STRmix can't grapple with that level of complexity by anyone's estimation.

Q So in so far as the person is trying to make an estimate or a guess, I guess, or an educated guess about whether two alleles at a particular locus pair up, extending that to the remaining loci that are reviewed, can you determine with certainty whether -- or with absolute certainty whether the two alleles that appear to be paired at locus one are contributed by the same individual that contributed two alleles at locus three? And same goes for locus four, locus five, locus six. Can you determine with absolute certainty that the same person donated all of those paired alleles at each locus?

A No.

Q Okay. And are the amounts that are present in an electropherogram, those are affected by the amplification process? I mean, that's the point of it, correct, to create more?

A The heights of the peaks are reflective. They are generally related to the amount of underlying DNA that was present. The smaller the amount of template DNA that you have

the greater the variability and the heights of the peaks that get amplified.

Q Okay. Thank you. We have heard testimony today about the potential impact of estimating the wrong number of contributors. Do you agree that if you wrongfully estimate or erroneously estimate the number of contributors, that that error is always without exception conservative and in favor of the defense?

A I don't think anyone says that it is always conservative. It's unquestionably not. We always in the published literature and Dr. Coble's testimony today, it's always got the qualifier typically we are generally or more often than not is conservative but it is not always.

The published literature shows clear instances where the exact opposite is the case, where underestimating the number of contributors leads to an attachment of undue weight to the failure to exclude somebody as a possible contributor.

Q And would one of those studies that you have just referenced, the Benschop article that was submitted to you in your preparation for your report in this case, which was Defendant Exhibit PP?

A Yes.

Q Thank you. I'd like to move to general acceptance. Is it your position that the relevant community for this consideration should involve more than just forensic

scientists?

A Absolutely.

Q Why?

A Well, I refer in my report to a paper or letter to the editor of the Journal of Forensic Science, that both I and Nathan Adams are cosigners to, that I think in a span of 10 or so paragraphs lays out the basis of my opinion there as to why it is that we need to have some breadth to the people who are involved in the relevant community to evaluate the general acceptance of complicated software like STRmix.

It's not just molecular biologists who are facile at isolating and purifying and amplifying DNA. It's not just population geneticists who have insights in terms of the rarity of a particular genotype or DNA profile. It needs to also include people who are familiar with the lessons that have been learned through the evaluation of software development and defects in software design, which is a very robust and well established discipline that again I think has some very valuable and important insights to add to this conversation.

Q I think in terms of general acceptance today was about the third time we used the airplane analogy, an airplane software analogy. And I see you made that same reference in page 6 of your report and you also stated at your deposition that you, quote, wouldn't be comfortable for my own purposes using any of what is currently available with respect to probabilistic

genotyping software programs. Do you feel the same way today?
A Well, first, I think we are double counting some of my allusions to airplanes. But the short answer to your question is, no, especially for a marginal sample, one where there is a relatively small amount of template, less than 50 picograms for instance, and where we're talking about a minor contributor, less than 10 percent for instance. I would be concerned about any of the existing software packages providing a statistical weight to the failure to exclude someone.

I think in the deposition it was suggested myself as a possible contributor to a mixture, and I want to say that Dr. Coble is exactly right in saying that CPI, the predecessor, the approach that was used prior to the advent of probabilistic genotyping, was a whole lot more problematic. And I have testified to that effect for longer than most and trying to draw attention to those potential problems.

Probabilistic genotyping is a step in the right direction, but I still don't think that we are at the point where we are, say, that it's a panacea for the entirety of the problem.

We heard Dr. Coble testify about how there has been an upswing in the marginal samples that are being submitted to crime laboratories. They are getting harder and harder to interpret to a large extent it's those ones at the edges that I think we need to be most worried about. There is some for

which STRmix I think unquestionably gives a great help, but the ones on the edges are the ones that I think we really need to be mindful of.

THE COURT: So Dr. Krane, if the Defendant in this case was identified as the 20 percent contributor, you wouldn't have any concern with the result? Is that what you are basically saying here?

THE WITNESS: Insofar as it pertained to the Defendant, yes, I would have no concern.

THE COURT: And if he was the 67 percent contributor would you be reasonably certain that the -- that he -- that the likelihood ratio was accurate?

THE WITNESS: I wouldn't have concern about the likelihood ratio being misinterpreted. Accurate for a likelihood ratio is a difficult concept.

THE COURT: I get that. I get that. Now I get that.

THE WITNESS: But you know, if the likelihood ratio was one in a billion, I would feel comfortable saying I know that this person is a contributor to this sample.

THE COURT: Okay.

THE WITNESS: In those circumstances.

THE COURT: And just one other thing, if I may? In reviewing your report, you suggested that an -- at 49 picograms that would amount to eight or nine human cells, is that -- is that correct? Do I get that right?

THE WITNESS: You do, yes.

THE COURT: All right.

THE WITNESS: And again, I think context there might be helpful to you in your work, and that is our bodies are made of trillions of cells, national debt kind of numbers of cells. And a typical fingerprint leaves behind on the order of 100 cells. And so the test results that we are talking about with the lowest of contributor in the evidence sample that seems to be at issue in this case is less than a tenth of what you might get from a casually placed fingerprint. It's a very small amount of small.

And by the same token, we had talked earlier about samples that appear to be derived from two or three picograms. Theoretically I am having a hard time wrapping my head around that because there is a suggestion that we are getting reliable DNA profile results from some fraction of a cell. Again, theoretically I have a hard time with that. And again, that seems inconsistent with what's been published in the literature about the lower bounds of what you need to be able to get a reliable result. One or two cells seems to be the lowest that I've seen in the published literature, not a fraction of a cell.

MS. KLOET: Thank you.

BY MR. KLOET:

Q To finish off on general acceptance, Dr. Krane, not all

probabilistic genotyping software is proprietary, correct? Some is open source and freely available?

A That's correct.

Q STRmix is a proprietary design such that developers and other program creators are not readily allowed access to these -- to this program. What do you think about that?

A I don't think it's a good system. I think it's not the way that things in the criminal justice system should be working. I am not a lawyer, but it seems to me like it's at odds with the constitutional premise that an accused be able to confront his accuser. And it seems to me that there is a tension that's in play between a right to a fair trial and int -- protection of intellectual property. I would have hoped that it is the trial aspects, the criminal trial aspects that would trump the intellectual property aspects, but that doesn't seem to be the way that the courts are moving on that particular issue.

Q From your understanding, Nathan Adams underwent a code review in this case of STRmix version 2.3.07, correct?

A I was a cosigner for the nondisclosure agreement associated with that review, yes.

Q Mr. Adams hasn't reviewed all the versions of STRmix, right?

A That's right.

Q In your opinion, based on what you know about the review and prior reviews he's done of STRmix, has a full, extensive,

thorough review of the STRmix source code been completed?
A Not even close.
Q Why is that?
A A thorough, comprehensive review would require thousands of people hours, maybe tens of thousands of people hours. Due to funding constraints and constraints of Nathan's time, nobody has conducted a review that's even close to that.
Q I am going to talk about section 5 now, application of STRmix in this case. Section 5 of your report. I think we have beaten this to death, but just to cap the day, as to number of contributors, is it possible that another analyst could have reached a different result than three contributors in this mixture in this case?
A You know, I didn't feel that I was specifically asked by the court to speak to the number of contributors. Apparently that's an important issue. I have heard quite a bit of questioning about that.

I feel very strongly that the most appropriate way to characterize the electropherograms and the evidence in this case is that it is a mixture of at least three contributors. Not three and only three contributors. Not even mostly three contributors. I would say that it is at least three, and I think there would be analysts who would look at these test results and disagree with me and say that it should be characterized at being at least four, not three, but rather at

least four.

So the short answer to your question is yes, different analysts may arrive at a different conclusion about the number of contributors.

Q Is there a chance that an analyst might mistakenly underestimate the number of contributors and believe honestly that a particular mixture falls within the boundaries of the validation study that was performed by their lab when in fact the number of contributors is higher than that estimate and therefore more complex and outside those boundaries?

A Yes.

Q Okay. In this case -- and I'll draw your attention to government Exhibit 8. This was a document I believe you were provided in preparation of your report. Can you identify what this is?

A Can I identify the document?

Q Or just describe what it is?

A Well, at the top it's an analysis run that was performed on a certain date for a particular evidence sample. And I recognize the evidence sample as the one that seems to be at issue in this case.

Q And what does this report tell you about the lowest contributors relative contribution?

A STRmix estimates that the lowest level contributor is contributing seven percent of the DNA to the sample.

Q And does this work sheet associate that particular contributor with the Defendant in this case?

A Yes.

Q Thank you. Did you have a chance to read Dr. Coble's report?

A I did.

Q Is there anything in that report that concerned you that you'd wish to discuss before the Court today beyond what we've already discussed?

A Well, that there is one thing that I would like to have a conversation with him about at some point after this is all settled, and that is the suggestion that this is a three-person mixture. I heard him today -- in his report he says he agrees with the analyst that it is a three-person mixture. In his testimony today I heard him say something that was more nuanced and I think more appropriate, and that is that it is apparently a three-person mixture. And in the context of forensic DNA profiling, that's a very important qualifier. Apparently would be consistent with my suggestion that it should be described as at least three contributors. That's different than saying that it is a three-person mixture. And I am afraid that a court might be easily misled by that type of language especially in a written report. And I just want to draw attention.

I know Dr. Coble knows better. He spoke to it today in his testimony, but I think his written report may have

benefitted from the inclusion of that word apparently or at least three contributors.

Q Thank you. Is there anything else that either you or Dr. Coble has testified to today or that the reports or the materials that have been offered to you to review as exhibits that you would like to discuss before we close?

A Well, there is one thing that I think might be -- I'd really like the Court to be mindful of. And I think it's something that Dr. Coble and I would agree to. And I -- in fact, I'd like to just read from a quote from something on which Dr. Coble is the lead author. And see, it's at the end of section 1 of my report. The first full paragraph. I think this is page 3.

My report says, similarly as pointed out by Dr. Coble in a 2016 publication, it's government's Exhibit 23, the goal of an internal validation study is to explore the limitation of the software and test the reliability, robustness and reproducibility of the system. Samples that mimic the types of cases encountered should be tested, close quote.

That same Coble, et al., 2016 paper goes onto say, quote, determination of the limits of the software is important to establish the types of profiles that are suitable for handling by the laboratory....probabilistic software, especially for low level DNA mixtures, may allow a laboratory to widen the scope of their case work in terms of the type of

evidence handled. However, there may also be a temptation to submit all complex mixtures to particularly versatile software. Therefore, the community is reminded of a previous recommendation of the DNA commission that is still valid, and that recommendation is, if the alleles of certain loci in the DNA profile are at a level that is dominated by background noise, then a biostatistical interpretation for those alleles should not be attempted.

As I look at the summary of the Michigan State Police validation work for STRmix, and at their protocols, I still do not see any clear articulation of what the limits for the use of STRmix should be. I see language that says that STRmix provided significant likelihood ratios for all quantities and mixture ratios evaluated. I don't think they have met that charge of articulating, of identifying boundaries at which analysts should either walk away or proceed with caution.

And as we have talked, it needs to be in conjunction. The quantity of template DNA, and the mixture ratio, I think we are all in agreement now that those are important considerations. I see no guidance along those lines.

And as I read the summary of the validation work that Michigan State Police did with STRmix, I find myself thinking -- and the Court has talked about independent validation. If I could, I'd like to just maybe put an asterisk there and say maybe not independent so much as a critical. I

don't know that I see evidence of a critical review.

I remember from my days as an undergraduate, I somehow or other stumbled into a business class, and there was a lecture about marketing where the only thing I remember from the whole class was essentially that the most avid reader of a Ford ad is a Ford owner. And if you stop to think about what that means is that you would have thought that Ford runs advertisements in magazines to persuade more people to buy Fords. The reality seems to have been, at least that insight is they were running ads to make Ford owners feel better about having purchased a Ford and feel, I want to go buy another Ford some time down the line.

That's what I find myself thinking is going on as I read this validation study. It seems to me that the Michigan State Police have been persuaded that STRmix is providing a useful answer to a very important question. How to attach a statistical weight to a mixed sample with an unknown number of contributors where allelic drop-out may have occurred. But it also seems to me that they haven't explored where it is that this promising tool fails to be reliable or helpful. They are embracing the shiny helpful aspects of the tool, but for a sample like the evidence sample in this case that's at the margins, I think we need to be mindful of the fact that it can't have -- it can't be all sunshine and roses. There must be some points at which STRmix isn't quite ready for prime

time. And I don't think the validation study from the Michigan State Police has identified what those circumstances are, what are the telltale signs that this is a sample that simply isn't suitable for use with this tool.

MS. KLOET: Thank you. No further questions.

THE COURT: I just have one, Dr. Krane. At the end of Dr. Coble's testimony I asked him whether there is some other new shiny tool out there ready to make a debut, and he essentially, I believe, and I hope I am not misinterpreting his comments, but his comment essentially was no, that into the foreseeable future probabilistic genotyping is it in terms of evaluating DNA sampling, and I am wondering whether you agree with that?

THE WITNESS: Probabilistic genotyping is unquestionably an improvement over what had been available before its arrival on the scene. No question about that. And I agree with Dr. Coble that for the foreseeable future probabilistic genotyping will be in play. I think the question, the point where perhaps he and I depart is it's obviously the case that I am more conservative about where it is to draw a line and say that the current probabilistic genotyping is -- has not yet been proven to be reliable. He seems to be willing to go further than I am.

I think he and I would both agree that as new versions of STRmix come out, and as improvements and refinements are

made to probabilistic genotyping in general, that the utility of the approach will only expand, but I think unfortunately for your sake, you need to decide are we at the edge of the reliability for the present iteration or are we -- is the edge somewhere on the other side.

THE COURT: Are we at the cutting edge or the bleeding edge?

THE WITNESS: Yes.

THE COURT: Okay. Thank you, very much, Dr. Krane. You may step down and I very much appreciate your testimony, as I did Dr. Coble's. It's extremely enlightening and very helpful.

THE WITNESS: Thank you.

(Witness excused, 3:54 p.m.)

THE COURT: I think that's it, Ladies and Gentlemen. I think that we are at the point where I have about as much information as I can digest. I think we have exhausted the subject, and unless there is something further, Mr. Presant?

MR. PRESANT: Your Honor, just what I offered before my filing and early in today's proceeding that we do have Lauren Lieu here from the Michigan State Police if the Court has questions for her. The government's exhibit has been admitted so I think it's before the Court.

THE COURT: It is.

MR. PRESANT: But I didn't want to miss the

opportunity if the Court had questions about that exhibit or the other information from the Michigan State Police to ask Ms. Lieu questions. I don't have any direct prepared for her.

THE COURT: I don't have anything further.

Ms. Kloet?

MS. KLOET: I have nothing further, Your Honor.

LAW CLERK: Can you confirm the exhibits that were admitted, or I can?

THE COURT: Why don't you do that.

LAW CLERK: Okay. I just want to confirm the exhibits that were admitted. I did not have Exhibit 39 for the government, so I have for the government Exhibits 33 through 38 and Exhibit 40.

MR. PRESANT: That's what I have.

LAW CLERK: Correct.

MR. PRESANT: Yeah.

LAW CLERK: And for the Defense Exhibit SS and TT.

MS. KLOET: Yes. And I think that Exhibit TT --

LAW CLERK: Was already admitted.

MS. KLOET: Thank you.

THE COURT: I have one further assignment for counsel. It's very apparent to me that you have both done the work that you should have in preparing for not only for the examinations of Dr. Coble and Dr. Krane but also in general. I think you have done a very good job of laying before the Court the issues

surrounding the evidence that the government wishes to admit against Mr. Gissantaner.

What I would like you to do, what I am ordering you to do is within the next 10 days -- well, let's make it two weeks. I want you to draft a document that lays out the 15 points that you believe were most significantly established in your favor in this testimony. Why do I pick 15? I have no idea. I started out at 10. That didn't seem like enough. Twenty seemed like too many. But I am very interested to know what you believe this testimony has established. It will be sort of I guess in the manner of a closing argument of sorts.

But it's important. I think there has been a lot of testimony here today. We had a lot of testimony from Dr. Buckleton, but I want you to concern yourself primarily with what we have heard today from Dr. Coble and Dr. Krane, who have really given us an awful lot to think about.

And if that is it, then, we will be adjourned. And you will see I am going to take this matter under advisement. I will certainly closely look at your submissions and I will have an opinion just as soon as we can. We are adjourned for today.

MR. PRESANT: Your Honor?

THE COURT: Yes.

MR. PRESANT: If I may, I am sorry, but just a couple questions on that last point.

THE COURT: Sure.

MR. PRESANT: First, I am going to be out of the office for the next week, so I was wondering if we could have more like three weeks for the submission?

THE COURT: Sure. Absolutely.

MR. PRESANT: Does Your Honor have a page limit or is it just 15 points?

THE COURT: Fifteen points and no more than five pages.

MS. KLOET: Thank you, Your Honor.

THE COURT: Thank you. Thank you, both.

LAW CLERK: All rise. Court is adjourned.

(Proceeding concluded, 3:58 p.m.)

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REPORTER'S CERTIFICATE

I, Paul G. Brandell, Official Court Reporter for the United States District Court for the Western District of Michigan, appointed pursuant to the provisions of Title 28, United States Code, Section 753, do hereby certify that the foregoing is a full, true and correct transcript of the proceedings had in the within entitled and numbered cause on the date hereinbefore set forth; and I do further certify that the foregoing transcript has been prepared by me or under my direction.

/s/ Paul G. Brandell

Paul G. Brandell, CSR-4552, RPR
U.S. District Court Reporter
399 Federal Building
Grand Rapids, Michigan 49503